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OM protein - protein search, using sw model

Run on: May 4, 2005, 12:07:58 ; Search time 121.5 Seconds
(without alignments)
28.649 Million cell updates/sec

Title: US-09-788-110A-1

Perfect score: 50

Sequence: 1 ILAKFLHWL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseqp16Dec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	9	3	AAY96327 HLA-A*020
2	50	100.0	9	3	AAY86846 Telomerases
3	50	100.0	9	3	AAY86846 Telomerases
4	50	100.0	9	3	AAB29461 Human tel
5	50	100.0	9	4	AAB73645 hTERT I54
6	50	100.0	9	4	AAB73645 hTERT I54
7	50	100.0	9	4	AAB73645 hTERT I54
8	50	100.0	9	4	AAB73645 hTERT I54
9	50	100.0	9	4	AAB73645 hTERT I54
10	50	100.0	9	5	ABG79085 Human HTR
11	50	100.0	9	5	ABG79084 Human HTR
12	50	100.0	9	5	ABG79084 Human HTR
13	50	100.0	9	5	ABG79084 Human HTR
14	50	100.0	9	5	ABG79084 Human HTR
15	50	100.0	9	6	ADA89161 hTERT der
16	50	100.0	9	7	AAC38655 HLA-A2 re
17	50	100.0	9	8	ADG89651 Class I H
18	50	100.0	9	8	ADG89650 Class I H
19	50	100.0	9	8	ADG89650 Class I H
20	50	100.0	9	8	ADG20364 Antigenic
21	50	100.0	9	8	ADG20364 Antigenic
22	50	100.0	9	8	ADG20364 Antigenic
23	50	100.0	10	5	ADG52357 HLA-A2 re
24	50	100.0	10	5	ADG52357 HLA-A2 re
25	50	100.0	10	5	ADG52357 HLA-A2 re
26	50	100.0	10	5	ADG52357 HLA-A2 re
27	50	100.0	10	5	ADG52357 HLA-A2 re
28	50	100.0	10	5	ADG52357 HLA-A2 re
29	50	100.0	10	5	ADG52357 HLA-A2 re
30	50	100.0	10	5	ADG52357 HLA-A2 re
31	50	100.0	10	5	ADG52357 HLA-A2 re
32	50	100.0	10	5	ADG52357 HLA-A2 re
33	50	100.0	10	5	ADG52357 HLA-A2 re
34	50	100.0	10	5	ADG52357 HLA-A2 re
35	50	100.0	10	5	ADG52357 HLA-A2 re
36	50	100.0	10	5	ADG52357 HLA-A2 re
37	50	100.0	10	5	ADG52357 HLA-A2 re
38	50	100.0	10	5	ADG52357 HLA-A2 re
39	50	100.0	10	5	ADG52357 HLA-A2 re
40	50	100.0	10	5	ADG52357 HLA-A2 re
41	50	100.0	10	5	ADG52357 HLA-A2 re
42	50	100.0	10	5	ADG52357 HLA-A2 re
43	50	100.0	10	5	ADG52357 HLA-A2 re
44	50	100.0	10	5	ADG52357 HLA-A2 re
45	50	100.0	10	5	ADG52357 HLA-A2 re

26	50	100.0	15	5	ABG71622	hTERT nes
27	50	100.0	17	5	ABG71624	hTERT pep
28	50	100.0	18	5	ABG71625	hTERT pep
29	50	100.0	19	5	ABG71626	hTERT pep
30	50	100.0	20	5	ABG71602	hTERT pep
31	50	100.0	100	5	ABG71628	hTERT fra
32	50	100.0	100	5	ABG71627	hTERT fra
33	50	100.0	291	6	AAO29774	hTERT MHC
34	50	100.0	437	2	AAO29774	hTERT MHC
35	50	100.0	438	2	AAO29774	hTERT MHC
36	50	100.0	500	6	AAO29840	Human CRT
37	50	100.0	514	2	AAW47004	Glutathio
38	50	100.0	588	2	AAO06644	N-termina
39	50	100.0	588	2	AAO06644	N-termina
40	50	100.0	617	2	AAO06636	N-termina
41	50	100.0	622	2	AAO06636	N-termina
42	50	100.0	807	2	AAW46997	Human CRT
43	50	100.0	807	2	AAO06637	N-termina
44	50	100.0	807	2	AAO06646	Truncated
45	50	100.0	936	2	AAO06651	Truncated

ALIGNMENTS

RESULT 1					
AAY96327					
ID	AAY96327 standard; peptide; 9 AA.				
XX					
AC	AAY96327;				
XX					
DT	29-AUG-2000 (first entry)				
XX					
DE	HLA-A*0201 binding peptide hTERT I540.				
XX					
KW	hTERT; telomerase complex; reverse transcriptase; MHC; HLA; CTL; cancer;				
KW	human leukocyte antigen; tumour-associated antigen; cytostatic; vaccine;				
KW	major histocompatibility complex; cytotoxic T lymphocyte; immunotherapy.				
XX					
OS	Homo sapiens.				
XX					
PN	WO200025813-A1.				
XX					
PD	11-MAY-2000.				
XX					
PF	29-OCT-1999; 99WO-US025438.				
XX					
PR	29-OCT-1998; 98US-0106106P.				
XX					
PA	(DAND) DANA FARBER CANCER INST INC.				
XX					
PI	(WHED) WHITEHEAD INST BIOMEDICAL RES.				
XX					
DR	Nadler LM, Hahn WC, Schultze JL, Vonderheide RH;				
XX					
XX	WPI; 2000-365402/31.				
PT	Universal tumor-associated antigens such as telomerase catalytic subunit				
XX					
PT	capable of binding major histocompatibility complex molecule useful for				
XX					
PS	diagnosis, prevention and treatment of cancer.				
XX					
CC	Claim 19; Page 58; 136pp; English.				
XX					
CC	Human telomerase complex reverse transcriptase (hTERT) is expressed in				
XX					
CC	more than 85 percent of human cancers. hTERT is useful as a universal				
XX					
CC	tumour-associated antigen (TAA) that binds to a major histocompatibility				
XX					
CC	complex molecule (MHC) hTERT peptides were analyzed for the ability to				
XX					
CC	bind to HLA (human leukocyte antigen) class I molecules. Cytotoxic T				
XX					
CC	lymphocytes (CTL) were then generated that kill a cell expressing hTERT				
XX					
CC	or a hTERT-TAA, in a hTERT or TAA specific MHC-restricted fashion.				
XX					
CC	Antigen presenting cells (APC) were also generated ex vivo for				
XX					
CC	presentation of a TAA peptide or hTERT. The APC can be used to activate				
XX					
CC	CTL to kill cells expressing the TAA. The TAA, hTERT peptides, APC and				
XX					
CC	CTL are useful for cancer immunotherapy. Measuring the level of CTL in a				

CC sample is useful for assessing the level of immunity of a patient to a
 CC TAA or a peptide, where the sample is obtained before or after a cancer
 CC treatment is given to the patient. TAA peptides (e.g. hTERT) are also
 CC useful for diagnosis and prophylactic treatment of cancer
 XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 50; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILAKFLHWL 9
 |||||
 Db 1 ILAKFLHWL 9

RESULT 2

RAY86646
 ID AAY86646 standard; peptide; 9 AA.

XX AC AAY86646;

DT 05-MAY-2000 (first entry)

DE Telomerase peptide #61.

XX Telomerase; antigenic peptide; cancer; therapy; human; tumour cell;
 KW malignant melanoma; leukaemia; lymphoma; biliary tract carcinoma;
 KW telomerase T lymphocyte.

XX Homo sapiens.

XX WO200002581-A1.

XX 20-JAN-2000.

PF 30-JUN-1999; 99WO-NO000220.

PR 08-JUL-1998; 98NO-00003141.

XX (NHVD) NORSK HYDRO AS.

PI Gaudernack G, Eriksen JA, Moller M, Gjertsen MK, Saeterdal I;
 PI Saeboe-Larsen S;

XX WPI; 2000-145727/13.

XX Protein or peptide fragments useful in the treatment and prophylaxis of
 PT cancer in mammals.

XX Claim 12; Page 35; 53pp; English.

XX This sequence represents a telomerase peptide of the invention, and can
 CC be used in a method for the treatment or prophylaxis of cancer. The
 CC sequences are useful in the treatment or prophylaxis of cancer
 CC especially, breast, lung, ovarian, cervical, colorectal, prostate or
 CC pancreatic cancers, malignant melanoma, leukaemias, lymphomas, or biliary
 CC tract carcinomas. They are useful for generating telomerase T lymphocytes
 CC capable of recognising and destroying tumour cells in a mammal,
 CC comprising culturing T lymphocytes obtained from the mammal with the
 CC peptides. Telomerase protein is expressed only by tumour cells, hence,
 CC other body cells are not targeted or destroyed by telomerase specific T
 CC cells. Note: This sequence was indexed from WO200002581, which is the
 CC first major country equivalent to NO9803141

XX Sequence 9 AA;

Query Match 100.0%; Score 50; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILAKFLHWL 9
 |||||

Db 1 ILAKFLHWL 9

RESULT 3

RAY86846
 ID AAY86846 standard; peptide; 9 AA.

XX AC AAY86846;

DT 05-MAY-2000 (first entry)

XX Telomerase peptide #261.

XX Telomerase; antigenic peptide; cancer; therapy; human; tumour cell;
 KW malignant melanoma; leukaemia; lymphoma; biliary tract carcinoma;
 KW telomerase T lymphocyte.

XX Homo sapiens.

XX WO200002581-A1.

XX 20-JAN-2000.

PF 30-JUN-1999; 99WO-NO000220.

PR 08-JUL-1998; 98NO-00003141.

XX (NHVD) NORSK HYDRO AS.

PI Gaudernack G, Eriksen JA, Moller M, Gjertsen MK, Saeterdal I;
 PI Saeboe-Larsen S;

XX WPI; 2000-145727/13.

XX Protein or peptide fragments useful in the treatment and prophylaxis of
 PT cancer in mammals.

XX Disclosure; Page 46; 53pp; English.

XX This sequence represents a telomerase peptide of the invention, and can
 CC be used in a method for the treatment or prophylaxis of cancer. The
 CC sequences are useful in the treatment or prophylaxis of cancer
 CC especially, breast, lung, ovarian, cervical, colorectal, prostate or
 CC pancreatic cancers, malignant melanoma, leukaemias, lymphomas, or biliary
 CC tract carcinomas. They are useful for generating telomerase T lymphocytes
 CC capable of recognising and destroying tumour cells in a mammal,
 CC comprising culturing T lymphocytes obtained from the mammal with the
 CC peptides. Telomerase protein is expressed only by tumour cells, hence,
 CC other body cells are not targeted or destroyed by telomerase specific T
 CC cells. Note: This sequence was indexed from WO200002581, which is the
 CC first major country equivalent to NO9803141

XX Sequence 9 AA;

Query Match 100.0%; Score 50; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILAKFLHWL 9
 |||||
 Db 1 ILAKFLHWL 9

RESULT 4

RAY29461
 ID AAB29461 standard; peptide; 9 AA.

XX AC AAB29461;

DT 09-FEB-2001 (first entry)

XX Human telomerase HLA-A2-binding antigen BPI-187.

KW Telomerase antigen; HLA-A2-binding; class I MHC; human leukocyte antigen;
 KW major histocompatibility complex; cytotoxic T-cell response;
 KW antigen-presenting cell; APC; telomerase-expressing cell; cancer;
 KW anticancer vaccine.
 XX
 OS Homo sapiens.
 XX
 PN WO200061766-A2.
 XX
 PD 19-OCT-2000.
 XX
 PF 07-APR-2000; 2000WO-IB000610.
 XX
 PR 09-APR-1999; 99US-0128539P.
 XX
 PA (BIOM-) BIOMIRA INC.
 XX
 FI Agrawal B, Longenecker BM;
 PI WPI; 2000-679493/66.
 DR
 XX New telomerase-specific T-cell antigens useful for generating T-cell
 PT responses against telomerases and for producing vaccines for treating or
 PT preventing cancer by in vivo or ex vivo techniques.
 XX
 PS Claim 4; Page 26; 34pp; English.
 XX
 CC The invention relates to a human telomerase peptide antigen (AAB29461)
 CC which binds to a class I HLA (human leukocyte antigen, MHC, major
 CC histocompatibility complex), and to conservatively substituted variants
 CC thereof. The invention also relates to a vaccine comprising a telomerase
 CC antigen or antigen variant, a nucleotide encoding a telomerase antigen or
 CC variant, and a method of producing telomerase-primed antigen-presenting
 CC cell (APC) comprising contacting an APC with a composition containing a
 CC telomerase antigen or variant. The telomerase antigens or vaccine
 CC compositions are useful for inducing a cytotoxic T-cell immune response
 CC against telomerase and hence against telomerase-expressing cells (i.e.,
 CC cancer cells. Additionally, the telomerase antigen-primed APC may be
 CC coadministered with interleukin-2 for cancer treatment or prevention. The
 CC present sequence represents a human telomerase HLA-A2-binding peptide
 CC antigen
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 50; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ILAKFLHWL 9
 Db 1 ILAKFLHWL 9
 RESULT 5
 AAB73645
 ID AAB73645 standard; peptide; 9 AA.
 XX
 AC AAB73645;
 XX
 DT 11-SEP-2001 (first entry)
 XX
 DE hTERT 1540 peptide.
 XX
 KW Cellular vaccine; antigen-presenting cell; APC;
 KW cell-surface molecule density; major histocompatibility complex; MHC;
 KW antigen-specific T-cell expansion; tumour; cancer; viral infection;
 KW parasitic infection; hTERT; 1540 peptide.
 XX
 OS Unidentified.
 XX
 PN WO200136978-A1.
 XX
 PD 25-MAY-2001.

XX 15-NOV-2000; 2000WO-US042213.
 XX
 PR 15-NOV-1999; 99US-0165428P.
 XX
 PA (DAND) DANA FARBER CANCER INST INC.
 XX
 PI Schultze JL, Vonderheide RH, Nadler LM, Maecker B;
 PI Von Bergwelt-Baildon M,
 XX WPI; 2001-343909/36.
 DR
 XX Determining surface density of molecules on antigen-presenting cells,
 PT useful for quality control of cellular vaccines for treatment of tumors
 PT and infections comprises measuring density ratios.
 XX
 PS Disclosure; Page 21; 47pp; English.
 XX
 CC The invention relates to a method of determining the surface density of a
 CC cell-surface molecule on a primary or artificial antigen-presenting cell
 CC (APC). The method comprises determining the cell surface area of the
 CC APCs, determining the absolute amount of cell surface molecule on the
 CC surface of the APCs, and calculating the ratio of the amount of the cell
 CC surface molecule to the APC surface area as a measure of cell surface
 CC molecule density. The invention also encompasses a kit for determining
 CC the cell-surface density of a complex of peptide and MHC (major
 CC histocompatibility complex) protein/peptide complex on an APC;
 CC identifying an agent that increases persistence of the MHC/peptide
 CC complex on an APC surface by culturing APCs in presence of test compound
 CC and measuring the time of persistence relative to an untreated control;
 CC and determining if the APC carries a therapeutically adequate amount of
 CC peptide by determining whether the cell-surface density of the
 CC MHC/peptide complex is 100 molecules/square micrometre or more. The
 CC method is used to determine if the amount of MHC/antigenic peptide
 CC complex present on the surface of an APC is sufficient for therapeutic
 CC use of the cells as cellular vaccines or for ex vivo expansion of antigen
 CC -specific T cells for subsequent return to the patient, particularly for
 CC the treatment of tumours or viral or parasitic infections. The method can
 CC also be used to identify agents that increase production of MHC/peptide
 CC complexes on cells, (which increases the therapeutic potential of the
 CC cells) by treatment before and/or during APC administration. The method
 CC allows identification of therapeutically useful antigen-pulsed APC
 CC optimisation of conditions for their production, and control of APC
 CC quality. Sequences AAB73643-AAB73648 represent peptides used in MHC
 CC binding studies and for the generation of peptide-specific cytotoxic T-
 CC lymphocytes
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 50; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ILAKFLHWL 9
 Db 1 ILAKFLHWL 9
 RESULT 6
 AAU07434
 ID AAU07434 standard; peptide; 9 AA.
 XX
 AC AAU07434;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Telomerase-derived peptide #3.
 XX
 KW MUC-1; mucin; cytostatic; virucide; vaccine; adjuvant peptide; antigen;
 KW immune response; cancer; viral disease; telomerase.
 XX
 OS Synthetic.

PN WO200170265-A2.
 XX 27-SEP-2001.
 PD 23-MAR-2001; 2001WO-IB000703.
 XX 24-MAR-2000; 2000US-0191736P.
 XX (BIOM-) BIOMIRA INC.
 PA Agrawal B, Longenecker MB, Parker J;
 PI WPI; 2001-611447/70.
 XX Novel vaccine for treating and preventing disorders such as cancer and
 PT viral diseases, comprises mucin MUC-1-based adjuvant peptide and an
 PT antigen.
 XX Example 2; Page 14; 22pp; English.
 PS The invention relates to a vaccine composition comprising a mucin MUC-1-
 CC based adjuvant peptide and an antigen. The vaccine composition is useful
 CC for stimulating the immune response of a patient, by administering the
 CC vaccine. Alternatively, this can be done by contacting ex vivo a T-cell
 CC from the patient with the vaccine and administering the contacted cells
 CC to the patient which stimulates the immune system of the patient. The
 CC vaccine is useful for treating and preventing disorders such as cancer
 CC and viral diseases. The vaccine is effective in generating an immune
 CC response to an antigen against which the patient does not respond. The
 CC present sequence represents the amino acid sequence of telomerase-
 CC derived peptide #3 which was used to determine antigen promiscuity of the
 CC vaccine composition
 XX Sequence 9 AA;
 SQ

Query Match 100.0%; Score 50; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILAKFLHWL 9
 |||||
 Db 1 ILAKFLHWL 9

RESULT 7
 AAB82772
 ID AAB82772 standard; protein; 9 AA.
 XX AAB82772;
 AC 29-OCT-2001 (first entry)
 DT Human telomerase reverse transcriptase peptide p540.
 DE Telomerase reverse transcriptase; hTERT; human; cancer; tumour;
 XX cytotoxic T lymphocyte; major histocompatibility complex;
 KW human leucocyte antigen; HLA-A2.1; vaccine.
 XX Homo sapiens.
 OS WO200160391-A1.
 FN 23-AUG-2001.
 PD 15-FEB-2001; 2001WO-US005143.
 PF 15-FEB-2000; 2000US-0182685P.
 XX 15-FEB-2001; 2001US-00182685.
 PR (REGC) UNIV CALIFORNIA.
 XX Zanetti M;
 PI

DR WPI; 2001-536552/59.
 XX Vaccine for initiating and enhancing a cytotoxic T lymphocyte response,
 PT for treating cancers or tumors or for inducing immune response against
 PT tumors, comprises a telomerase reverse transcriptase peptide.
 XX Example 1; Page 12; 52pp; English.
 PS The present sequence is that of human telomerase reverse transcriptase
 CC (hTERT) peptide p540, comprising a human leukocyte antigen HLA-A2.1
 CC molecule binding motif corresponding to amino acid residues 540-548 of
 CC hTERT (see AAB827765). Analysis showed that the majority of healthy
 CC individuals as well as patients with prostate cancer immunised in vitro
 CC against p540 or p865 (see AAB82773) developed hTERT-specific cytotoxic T
 CC lymphocytes (CTL). The cancer patients' CTL specifically lysed a variety
 CC of HLA-A2+ cancer cell lines such as prostate, breast, colon, lung and
 CC melanoma, demonstrating immunological recognition of endogenously
 CC processed hTERT peptides. In vivo immunisation of HLA-A2.1 transgenic mice
 CC generated a specific CTL response against both hTERT peptides. The
 CC induction of CTL responses in vitro and in vivo, and the susceptibility
 CC to lysis of tumour cells of various origins by hTERT CTL suggest that hTERT
 CC could serve as a universal cancer vaccine for humans. Thus, a claimed
 CC universal vaccine for treating tumours of any origin comprises at least 1
 CC hTERT peptide in an amount effective for initiating and enhancing a CTL in
 CC response against cancer cells. The peptide is 7-15 amino acid residues in
 CC length and may be modified to enhance binding to the major
 CC histocompatibility complex. Also claimed is a method for inducing and
 CC enhancing a CTL response against cancer cells, involving harvesting blood
 CC leucocytes, pulsing with hTERT, and contacting cancer cells with the
 CC pulsed leucocytes. A method for targeting CTL to tumour cells is also
 CC claimed, and involves administering a hTERT peptide to a mammal,
 CC especially a cancer patient
 XX Sequence 9 AA;
 SQ

Query Match 100.0%; Score 50; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILAKFLHWL 9
 |||||
 Db 1 ILAKFLHWL 9

RESULT 8
 AAM07000
 ID AAM07000 standard; peptide; 9 AA.
 XX AAM07000;
 AC 09-OCT-2001 (first entry)
 DT hTERT 1540 peptide.
 DE Cytochrome P450 1B1; CYP1B1; cancer; immunotherapy; diagnosis; HLA;
 XX human leukocyte antigen; cytotoxic T-lymphocyte; CTL; MHC; APC;
 KW major histocompatibility complex; antigen presenting cell; melanoma;
 XX lymphoma; carcinoma; sarcoma; multiple myeloma; leukaemia.
 OS Homo sapiens.
 FN WO200135810-A2.
 XX 25-MAY-2001.
 PD 15-NOV-2000; 2000WO-US031513.
 PF 15-NOV-1999; 99US-0165590P.
 XX (DAND) DANA FARBER CANCER INST INC.
 XX (UYBO-) UNIV BOSTON.
 XX Schultze JL, Vonderheide RH, Sherr D, Nadler LM, Maecker B;
 PI

PI Von Bergwelt- Baildon M;
 XX WPI; 2001-355537/37.
 XX
 PT Treating a cancer patient involves administering to patient a cytotoxic T
 PT -lymphocyte, an antigen presenting cell that activates T cells, a peptide
 PT of cytochrome P450 1B1, or a polynucleotide encoding the peptide.
 XX
 XX Disclosure; Page 42; 121pp; English.
 XX
 CC The present invention describes a method for treating a patient having,
 CC or is at risk of having, a cell expressing cytochrome P450 1B1 (CYP1B1),
 CC which involves administering to the patient a cytotoxic T-lymphocyte
 CC (CTL) that kills the cell, an antigen presenting cell (APC) that
 CC activates CTL, a peptide of CYP1B1 that binds to major histocompatibility
 CC complex (MHC) molecule, or a nucleic acid molecule encoding CYP1B1 or
 CC peptide of CYP1B1. Also described are: (1) a method for assessing the
 CC level of immunity of a patient to CYP1B1 or a peptide of CYP1B1 that
 CC binds to MHC complex molecule, involving measuring the level of CTL
 CC specific for CYP1B1 or the peptide of CYP1B1 in a sample from the patient
 CC ; (2) a CYP1B1 peptide (I) that binds to MHC complex molecule; (3) an ex
 CC vivo generated CTL (II) that specifically kills a cell expressing CYP1B1
 CC in a specific of a MHC complex-restricted fashion; and (4) an ex vivo
 CC generated APC (III) that presents a peptide of a CYP1B1 in the context of
 CC a MHC complex molecule. The method is useful for treating a patient
 CC having or is at risk of having a cell that expresses CYP1B1. The method
 CC is useful for the prevention, treatment and diagnosis of cancer, e.g.
 CC melanoma, lymphoma, carcinoma, sarcoma, multiple myeloma, leukemia, and
 CC lung, ovarian, uterine, cervical, prostate, liver, colon, pancreatic and
 CC brain cancer. AAM06905 to AAM13566 represent CYP1B1 peptides which can
 CC bind to human leukocyte antigens (HLA), as well as other amino acid
 CC sequence used in the exemplification of the present invention
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 50; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ILAKFLHWL 9
 Db 1 ILAKFLHWL 9
 RESULT 9
 ABG79085
 ID ABG79085 standard; peptide; 9 AA.
 AC ABG79085;
 XX
 XX 15-NOV-2002 (first entry)
 DT
 DE Human HTRT class I HLA widely expressed antigen peptide #1.
 KW Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen;
 KW lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia;
 KW Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
 KW kidney cancer; adenocarcinoma; breast cancer; prostate cancer;
 KW ovarian cancer; pancreatic cancer; epitope; vaccine; dendritic cell;
 KW tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
 KW cytostatic; human.
 XX
 OS Homo sapiens.
 XX
 XX WO200264057-A2.
 FN
 PD 22-AUG-2002.
 XX
 XX 15-FEB-2002; 2002WO-US005212.
 PF
 XX 15-FEB-2001; 2001US-0268687P.
 PR
 XX (BAYU) BAYLOR COLLEGE MEDICINE.
 PA

XX Wang R;
 PI
 XX WPI; 2002-627577/67.
 DR
 XX Novel composition for treating a disease in an animal, comprises an
 PT immune effector cell and cell penetrating peptide associated with an
 PT antigen or antibody.
 PT
 XX Disclosure; Page 18; 61pp; English.
 PS
 XX The invention relates to a composition (I) comprising an immune effector
 CC cell and a cell penetrating peptide (CPP) associated with an antigen or
 CC antibody. Also included are (1) a vaccine comprising (I), CPP associated
 CC with an antigen, and a pharmaceutically acceptable carrier and (2)
 CC preparing a composition for a disease, by providing (I) and CPP
 CC associated with an antigen for disease, and introducing the antigen-
 CC associated CPP to (I), where antigen enters into the cell. The antigens
 CC are, for example, tumour antigen derived epitopes recognised by tumour
 CC infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I
 CC or II. The composition is useful for enhancing immunity in an animal to a
 CC disease, by administering a mature dendritic cell comprising CPP
 CC associated with an antigen to disease, to the animal, such that following
 CC the administration, animal is protected from disease, where the animal
 CC comprises both CD4+ and CD8+ T cells. It is also useful for treating a
 CC disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung
 CC cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine
 CC cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma,
 CC breast cancer, prostate cancer, ovarian cancer and pancreatic cancer).
 CC The animal is further subjected to a cancer treatment including surgery,
 CC radiation, chemotherapy or gene therapy. The administration of (I),
 CC preferably dendritic cell is prior to, subsequent to or concurrent with,
 CC the cancer treatment. The present sequence is a tumour antigen derived
 CC epitope for inclusion in the composition of the invention
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 50; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ILAKFLHWL 9
 Db 1 ILAKFLHWL 9
 RESULT 10
 ABG79084
 ID ABG79084 standard; peptide; 9 AA.
 XX
 AC ABG79084;
 XX
 XX 15-NOV-2002 (first entry)
 DT
 DE Human HTEXT class I HLA widely expressed antigen peptide #1.
 XX
 KW Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen;
 KW lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia;
 KW Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
 KW kidney cancer; adenocarcinoma; breast cancer; prostate cancer;
 KW ovarian cancer; pancreatic cancer; epitope; vaccine; dendritic cell;
 KW tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
 KW cytostatic; human.
 XX
 OS Homo sapiens.
 XX
 XX WO200264057-A2.
 FN
 PD 22-AUG-2002.
 XX
 XX 15-FEB-2002; 2002WO-US005212.
 PF
 XX 15-FEB-2001; 2001US-0268687P.
 PR
 XX (BAYU) BAYLOR COLLEGE MEDICINE.
 PA

XX PA (BAYU) BAYLOR COLLEGE MEDICINE.
 XX PI Wang R;
 XX DR WPI; 2002-627577/67.
 XX PT Novel composition for treating a disease in an animal, comprises an
 PT immune effector cell and cell penetrating peptide associated with an
 PT antigen or antibody.
 XX PS Disclosure; Page 18; 61pp; English.
 XX CC The invention relates to a composition (I) comprising an immune effector
 CC cell and a cell penetrating peptide (CPP) associated with an antigen or
 CC antibody. Also included are (i) a vaccine comprising (I). CPP associated
 CC with an antigen, and a pharmaceutically acceptable carrier and (2)
 CC preparing a composition for a disease, by providing (I) and CPP
 CC associated with an antigen for disease, and introducing the antigen-
 CC associated CPP to (I), where antigen enters into the cell. The antigens
 CC are, for example, tumour antigen derived epitopes recognised by tumour
 CC infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I
 CC or II. The composition is useful for enhancing immunity in an animal to a
 CC disease, by administering a mature dendritic cell comprising CPP
 CC associated with an antigen to disease, to the animal, such that following
 CC the administration, animal is protected from disease, where the animal
 CC comprises both CD4+ and CD8+ T cells. It is also useful for treating a
 CC disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung
 CC cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine
 CC cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma,
 CC breast cancer, prostate cancer, ovarian cancer and pancreatic cancer).
 CC The animal is further subjected to a cancer treatment including surgery,
 CC radiation, chemotherapy or gene therapy. The administration of (I),
 CC preferably dendritic cell is prior to, subsequent to or concurrent with,
 CC the cancer treatment. The present sequence is a tumour antigen derived
 CC epitope for inclusion in the composition of the invention
 XX SQ Sequence 9 AA;
 Query Match 100.0%; Score 50; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ILAKFLHWL 9
 Db |||||
 1 ILAKFLHWL 9
 RESULT 12
 AAE26818
 ID AAE26818 standard; peptide; 9 AA.
 AC AAE26818;
 XX 13-DEC-2002 (first entry)
 DT Human HLA-A2.1 restricted telomerase peptide epitope #1.
 XX Human; cancer; breast cancer; ovarian cancer; melanoma; cell therapy;
 KW epitope; human leucocyte antigen; HLA-A2.1.
 XX Homo sapiens.
 OS WO200265992-A2.
 PN 29-AUG-2002.
 PD 19-FEB-2002; 2002WO-US005748.
 PF 20-FEB-2001; 2001US-0270252P.
 PR (ORTH) ORTHO-MCNEIL PHARM INC.
 PA Degraw J, Moriarty A, Leturcq DJ, Jackson MR, Peterson PA;
 PI Heiskala M;
 PI WPI; 2002-667033/71.
 DR Treating a subject with cancer comprises combining the CD+8 cells, which
 XX are stimulated with non-naturally occurring antigen-presenting cell line,
 PT with adherent blood monocytes and inoculating the subject with CD8+
 PT suspension.
 XX Example 2; Page 97; 99pp; English.
 PS The invention relates to a method of treating a subject with cancer. The
 CC method involves combining the CD+8 cells, which are stimulated with non
 CC naturally occurring antigen-presenting cell (mAPC) line, with adherent
 CC blood monocytes and inoculating the subject with CD8+ suspension. The
 CC method is useful for treating cancer e.g. ovarian cancer, breast cancer
 CC and melanoma etc. It is also useful in cell therapy. The present sequence
 CC is human leukocyte antigen A2 (HLA-A2).1 restricted peptide epitope used
 CC to treat breast and ovarian cancer

XX PA (BAYU) BAYLOR COLLEGE MEDICINE.
 XX PI Wang R;
 XX DR WPI; 2002-627577/67.
 XX PT Novel composition for treating a disease in an animal, comprises an
 PT immune effector cell and cell penetrating peptide associated with an
 PT antigen or antibody.
 XX PS Disclosure; Page 18; 61pp; English.
 XX CC The invention relates to a composition (I) comprising an immune effector
 CC cell and a cell penetrating peptide (CPP) associated with an antigen or
 CC antibody. Also included are (i) a vaccine comprising (I). CPP associated
 CC with an antigen, and a pharmaceutically acceptable carrier and (2)
 CC preparing a composition for a disease, by providing (I) and CPP
 CC associated with an antigen for disease, and introducing the antigen-
 CC associated CPP to (I), where antigen enters into the cell. The antigens
 CC are, for example, tumour antigen derived epitopes recognised by tumour
 CC infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I
 CC or II. The composition is useful for enhancing immunity in an animal to a
 CC disease, by administering a mature dendritic cell comprising CPP
 CC associated with an antigen to disease, to the animal, such that following
 CC the administration, animal is protected from disease, where the animal
 CC comprises both CD4+ and CD8+ T cells. It is also useful for treating a
 CC disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung
 CC cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine
 CC cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma,
 CC breast cancer, prostate cancer, ovarian cancer and pancreatic cancer).
 CC The animal is further subjected to a cancer treatment including surgery,
 CC radiation, chemotherapy or gene therapy. The administration of (I),
 CC preferably dendritic cell is prior to, subsequent to or concurrent with,
 CC the cancer treatment. The present sequence is a tumour antigen derived
 CC epitope for inclusion in the composition of the invention
 XX SQ Sequence 9 AA;
 Query Match 100.0%; Score 50; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ILAKFLHWL 9
 Db |||||
 1 ILAKFLHWL 9
 RESULT 11
 ABB76784
 ID ABB76784 standard; peptide; 9 AA.
 AC ABB76784;
 XX 31-MAY-2002 (first entry)
 DT Telomerase epitope hp540 presented by HLA A2.1.
 DE Antiviral; anti-HIV; cytostatic; epitope; HLA A2.1;
 KW human leukocyte antigen; immunotherapy; cancer; viral infection; vaccine.
 XX Unidentified.
 OS FR2812087-A1.
 PN 25-JAN-2002.
 PD 21-JUL-2000; 2000FR-00009591.
 PF 21-JUL-2000; 2000FR-00009591.
 PR (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PA

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 50; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILAKFLHWL 9
 Db 1 ILAKFLHWL 9

RESULT 13
 ABG71603
 ID ABG71603 standard; peptide; 9 AA.
 XX AC ABG71603;
 XX XX
 DT 09-JAN-2003 (first entry)
 XX XX
 DE hTERT nested HLA class I epitope #1.
 XX XX
 KW Human; telomerase catalytic subunit; hTERT; human leukocyte antigen;
 KW human telomerase reverse transcriptase; HLA epitope; cancer; HLA profile;
 KW breast cancer; pancreatic cancer; colorectal cancer; lung cancer;
 KW ovarian cancer; cervical cancer; malignant melanoma; leukaemia; lymphoma;
 KW biliary tract carcinoma; anti-cancer; cytostatic; HLA class I epitope.
 XX XX
 OS Homo sapiens.
 XX XX
 PN WO200270679-A2.
 XX XX
 PD 12-SEP-2002.
 XX XX
 PF 19-FEB-2002; 2002WO-N0000069.
 XX XX
 PR 02-MAR-2001; 2001GB-00005238.
 XX XX
 PA (GEWV-) GEWVX AS.
 XX XX
 PI Eriksen JA, Gaudernack G, Moller M;
 XX XX
 DR WPI; 2002-750459/81.
 XX XX
 FT New polypeptide with an additional C-terminal and/or N-terminal sequence,
 PT useful for preparing anti-cancer vaccines.
 XX XX
 PS Example 1; Page 28; 62pp; English.
 XX XX
 CC The present invention relates to a polypeptide comprising a 20 amino acid
 CC sequence derived from human telomerase catalytic subunit (or human
 CC telomerase reverse transcriptase, hTERT) amino acid residues 537-556, or
 CC fragments thereof comprising at least 10 amino acids and at least two
 CC human leukocyte antigen (HLA) class I or class II epitopes. The invention
 CC also describes a polypeptide having the above 20 amino acid peptide
 CC sequence as additional C- and/or N-terminal sequences on a fragment of
 CC hTERT which is not more than 100 amino acids of hTERT. The polypeptides
 CC of the invention are useful in a pharmaceutical composition or in a
 CC vaccine for preventing or treating cancer in populations of individuals
 CC having varying HLA profiles. The polypeptides are also useful in a
 CC diagnostic kit for diagnosing cancers such as breast, pancreatic,
 CC colorectal, lung, ovarian or cervical cancer, malignant melanoma,
 CC leukaemia, lymphoma or biliary tract carcinoma. The polypeptides or
 CC encoding polynucleotide sequences are useful for performing identity,
 CC sequence homology and/or hybridisation studies, for predicting structure
 CC and/or function (e.g. anti-cancer activity), or for screening methods in
 CC drug development or drug screening procedures. ABG71603-ABG71619
 CC represent hTERT peptides containing nested HLA class I epitopes
 XX XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 50; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILAKFLHWL 9
 Db 1 ILAKFLHWL 9

RESULT 14
 ABR39878
 ID ABR39878 standard; peptide; 9 AA.
 XX AC ABR39878;
 XX XX
 DT 11-AUG-2003 (first entry)
 XX XX
 DE Peptide having relative affinity to hTERT antigen.
 XX XX
 KW Protein function; tumour; immunotherapy; diagnosis; hTERT; HER-2/neu;
 KW PSMA; NPM/ALK.
 XX XX
 OS Synthetic.
 XX XX
 PN WO2003015001-A2.
 XX XX
 PD 20-FEB-2003.
 XX XX
 PF 15-JUL-2002; 2002WO-GB003244.
 XX XX
 PR 03-AUG-2001; 2001EP-00402106.
 XX XX
 PA (SYNT-) SYNT-EM SA.
 XX XX
 PI Giraud E, Gomar J, Kosmatopoulos K, Lahana R, Rees A;
 XX XX
 DR WPI; 2003-256630/25.
 XX XX
 FT Determining functions of protein sequences using computational methods,
 PT useful, for example, in tumor and virus immunotherapy and/or diagnosis.
 XX XX
 PS Example; Page 34; 47pp; English.
 XX XX
 CC The invention relates to determining if a query protein (P) sequence has
 CC a functional property of interest, by providing a dataset of (P)'s that
 CC share the functional property of interest, determining for each (P) at
 CC least one frameset, encoding many physicochemical and/or topological
 CC descriptor parameters (PAS) for each frameset. The frameset in the method
 CC is a region within the (P) which imparts to the (P) the functional
 CC property of interest. The descriptor (PAS) are indicative of the
 CC functional property of interest. The methods and compositions are useful,
 CC e.g., in tumour and virus immunotherapy and diagnosis. Sequences ABR39871
 CC -918 represent peptides selected by the SCIPS model, showing relative
 CC affinity to various antigens like hTERT, HER-2/neu, PSMA and NPM/ALK
 XX XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 50; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILAKFLHWL 9
 Db 1 ILAKFLHWL 9

RESULT 15
 ADA89161
 ID ADA89161 standard; peptide; 9 AA.
 XX AC ADA89161;
 XX XX
 DT 20-NOV-2003 (first entry)
 XX XX
 DE hTERT derived peptide T540 SEQ ID NO:5.

XX immunoglobulin; Ig; heavy chain variable domain;
 KW light chain variable domain; major histocompatibility complex; MHC;
 KW gp100; MUC1; TAX; hTERT; cytostatic; gene therapy; cancerous disorder;
 KW cancer; gene; ds.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO2003070752-A2.
 XX
 PD 28-AUG-2003.
 XX
 PF 20-FEB-2003; 2003WO-US005128.
 XX
 PR 20-FEB-2002; 2002US-0358994P.
 XX
 PA (DYAX-) DYAX CORP.
 PA (TECR) TECHNION RES & DEV FOUND LTD.
 XX
 PI Hoogenboom HRJM, Reiter Y;
 XX
 DR WPI; 2003-663847/62.
 XX
 PT New protein comprising an immunoglobulin heavy chain variable (VH) domain
 PT and an immunoglobulin light chain variable (VL) domain, useful for
 PT preparing a composition for treating or preventing a cancerous disorder.
 XX
 PS Claim 3; Page 137; 224pp; English.
 XX
 CC The present invention describes a protein comprising an immunoglobulin
 CC (Ig) heavy chain variable (VH) domain and an Ig light chain variable (VL)
 CC domain. The protein binds a complex comprising a major histocompatibility
 CC complex (MHC) and a peptide, does not substantially bind the MHC in the
 CC absence of the bound peptide, and does not substantially bind the peptide
 CC in the absence of the MHC. The peptide is a peptide fragment of gp100,
 CC MUC1, TAX or hTERT. Also described: (1) a pharmaceutical composition
 CC comprising the novel protein and a carrier; (2) a cytotoxic T cell
 CC comprising one or more nucleic acids for expressing the Ig that binds a
 CC complex having an MHC and a peptide, does not substantially bind the MHC
 CC in the absence of the bound peptide, and does not substantially bind the
 CC peptide in the absence of the MHC; (3) an isolated nucleic acid
 CC comprising a first segment that encodes the Ig variable domain; (4) a
 CC host cell comprising heterologous nucleic acid sequences that encodes the
 CC novel protein; (5) a transgenic animal whose genome includes heterologous
 CC nucleic acid sequences that encode the protein; (6) identifying the
 CC protein that specifically binds the MHC-peptide complex; (7) expressing
 CC an antigen-binding protein; (8) ablating or killing a target cell that
 CC displays a peptide on a surface MHC molecule; (9) treating or preventing
 CC a cancerous disorder in a subject; and (10) detecting an MHC-peptide
 CC complex in a sample. A protein of the invention has cytostatic activity,
 CC and can be used in gene therapy. The protein is useful for preparing a
 CC composition for treating or preventing a cancerous disorder. The present
 CC sequence represents a hTERT-derived peptide, which is used in the
 CC exemplification of the present invention.
 XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 50; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILAKFLHWL 9
 |||||
 Db 1 ILAKFLHWL 9

Search completed: May 4, 2005, 12:24:14
 Job time : 123.5 secs

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OM protein - protein search, using sw model

Run on: May 4, 2005, 12:07:58 ; Search time 121.5 Seconds
(without alignments)
28.649 Million cell updates/sec

Title: US-09-788-110A-2

Perfect score: 43

Sequence: 1 RLVDPLIV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:*
1: geneseqp1980a:*
2: geneseqp1990a:*
3: geneseqp2000a:*
4: geneseqp2001a:*
5: geneseqp2002a:*
6: geneseqp2003a:*
7: geneseqp2003bs:*
8: geneseqp2004a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	9	3 AAY96329	HLA-A*020
2	43	100.0	9	3 AAY86628	Telomeras
3	43	100.0	9	3 AAY86650	Telomeras
4	43	100.0	9	3 AAB29462	HLA-A2-as
5	43	100.0	9	4 AAU07432	Telomeras
6	43	100.0	9	4 AAB82773	Human tel
7	43	100.0	9	5 ABG79086	Human HTR
8	43	100.0	9	5 AAE26819	Human HLA
9	43	100.0	9	5 AAE17299	Human leu
10	43	100.0	9	6 ADA89162	hTERT der
11	43	100.0	9	7 AAE38656	HLA-A2 re
12	43	100.0	9	8 ADG89652	Class I H
13	43	100.0	9	8 ADS52358	HLA-A2 re
14	43	100.0	10	3 AAY96397	HLA-A2 bi
15	43	100.0	13	3 AAY86591	Telomeras
16	43	100.0	17	3 AAY86598	Telomeras
17	43	100.0	17	6 AAO29827	hTERT MHC
18	43	100.0	174	6 AAO29775	hTERT MHC
19	43	100.0	436	6 ABB99680	Splice va
20	43	100.0	438	2 AAY25462	Human CRT
21	43	100.0	456	8 ADG70126	HIV RT/ht
22	43	100.0	462	8 ADG70124	HIV RT/ht
23	43	100.0	463	6 ABB99679	Splice va
24	43	100.0	499	6 ABB99678	Amino aci
25	43	100.0	500	6 AAO29840	Human tel

26	43	100.0	538	2 AAW47001	Glutathio
27	43	100.0	564	2 AAW56109	Human tel
28	43	100.0	576	8 ADG70112	HIV-1 RT/
29	43	100.0	586	8 ADG70131	HIV RT/ht
30	43	100.0	586	8 ADG70125	HIV RT/ht
31	43	100.0	591	2 AAW97384	A catalyt
32	43	100.0	592	8 ADG70120	HIV RT/ht
33	43	100.0	592	8 ADG70123	HIV RT/ht
34	43	100.0	605	8 ADG70122	HIV RT/ht
35	43	100.0	605	8 ADG70121	HIV RT/ht
36	43	100.0	622	2 AAY25463	Human CRT
37	43	100.0	803	8 ADG70134	HIV RT/ht
38	43	100.0	816	8 ADG70135	HIV RT/ht
39	43	100.0	816	8 ADG70132	HIV RT/ht
40	43	100.0	816	8 ADG70133	HIV RT/ht
41	43	100.0	867	4 AAE00424	Candida a
42	43	100.0	867	4 AAE00423	Candida a
43	43	100.0	867	7 ADD21426	C albican
44	43	100.0	936	2 AAY00651	Truncated
45	43	100.0	936	2 AAY00642	Truncated

ALIGNMENTS

RESULT 1
AAY96329
ID AAY96329 standard; peptide; 9 AA.
XX
AC AAY96329;
XX
DT 29-AUG-2000 (first entry)
XX
DE HLA-A*0201 binding peptide hTERT R865.
XX
KW hTERT; telomerase complex; reverse transcriptase; MHC; HLA; CTL; cancer;
KW human leukocyte antigen; tumour-associated antigen; cytostatic; vaccine;
KW major histocompatibility complex; cytotoxic T lymphocyte; immunotherapy.
XX
OS Homo sapiens.
XX
PN WO200025813-A1.
XX
PD 11-MAY-2000.
XX
PF 29-OCT-1999; 99WO-US025438.
XX
PR 29-OCT-1998; 98US-0106106P.
XX
PA (DAND) DANA PARBER CANCER INST INC.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PI Nadler LM, Hahn WC, Schultze JL, Vonderheide RH;
DR WPI; 2000-365402/31.
XX
PT Universal tumor-associated antigens such as telomerase catalytic subunit
PT capable of binding major histocompatibility complex molecule useful for
PT diagnosis, prevention and treatment of cancer.
XX
PS Disclosure; Page 59; 136pp; English.
XX
CC Human telomerase complex reverse transcriptase (hTERT) is expressed in
CC more than 85 percent of human cancers. hTERT is useful as a universal
CC tumour-associated antigen (TAA) that binds to a major histocompatibility
CC complex molecule (MHC) hTERT peptides were analyzed for the ability to
CC bind to HLA (human leukocyte antigen) class I molecules. Cytotoxic T
CC lymphocytes (CTL) were then generated that kill a cell expressing hTERT
CC or a hTERT-TAA, in a hTERT or TAA specific MHC-restricted fashion.
CC Antigen presenting cells (APC) were also generated ex vivo for
CC presentation of a TAA peptide or hTERT. The APC can be used to activate
CC CTL to kill cells expressing the TAA. The TAA, hTERT peptides, APC and
CC CTL are useful for cancer immunotherapy. Measuring the level of CTL in a

CC sample is useful for assessing the level of immunity of a patient to a
 CC TAA or a peptide, where the sample is obtained before or after a cancer
 CC treatment is given to the patient. TAA peptides (e.g. hTERT) are also
 CC useful for diagnosis and prophylactic treatment of cancer

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 43; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLVDFFLLV 9
 |||||

Db 1 RLVDFFLLV 9
 |||||

RESULT 2

RAY86628
 ID AAY86628 standard; peptide; 9 AA.

XX AC AAY86628;

XX DT 05-MAY-2000 (first entry)

XX DE Telomerase peptide #43.

XX KW Telomerase; antigenic peptide; cancer; therapy; human; tumour cell;
 KW malignant melanoma; leukaemia; lymphoma; biliary tract carcinoma;
 KW telomerase T lymphocyte.

XX OS Homo sapiens.

XX PN WO200002581-A1.

XX PD 20-JAN-2000.

XX PF 30-JUN-1999; 99WO-NO000220.

XX PR 08-JUL-1998; 98NO-00003141.

XX PA (NHVD) NORSE HYDRO AS.

XX PI Gaudernack G, Eriksen JA, Moller M, Gjertsen MK, Saeterdal I;
 PI Saebøe-Larsen S;

XX DR WPI; 2000-145727/13.

XX PT Protein or peptide fragments useful in the treatment and prophylaxis of
 PT cancer in mammals.

XX PS Claim 10; Page 34; 53pp; English.

XX CC This sequence represents a telomerase peptide of the invention, and can
 CC be used in a method for the treatment or prophylaxis of cancer. The
 CC sequences are useful in the treatment or prophylaxis of cancer
 CC especially, breast, lung, ovarian, cervical, colorectal, prostate or
 CC pancreatic cancers, malignant melanoma, leukaemias, lymphomas, or biliary
 CC tract carcinomas. They are useful for generating telomerase T lymphocytes
 CC capable of recognising and destroying tumour cells in a mammal,
 CC comprising culturing T lymphocytes obtained from the mammal with the
 CC peptides. Telomerase protein is expressed only by tumour cells, hence,
 CC other body cells are not targeted or destroyed by telomerase specific T
 CC cells. Note: This sequence was indexed from WO200002581, which is the
 CC first major country equivalent to NO9803141

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 43; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLVDFFLLV 9
 |||||

Db 1 RLVDFFLLV 9

RESULT 3

RAY86650
 ID AAY86650 standard; peptide; 9 AA.

XX AC AAY86650;

XX DT 05-MAY-2000 (first entry)

XX DE Telomerase peptide #65.

XX KW Telomerase; antigenic peptide; cancer; therapy; human; tumour cell;
 KW malignant melanoma; leukaemia; lymphoma; biliary tract carcinoma;
 KW telomerase T lymphocyte.

XX OS Homo sapiens.

XX PN WO200002581-A1.

XX PD 20-JAN-2000.

XX PF 30-JUN-1999; 99WO-NO000220.

XX PR 08-JUL-1998; 98NO-00003141.

XX PA (NHVD) NORSE HYDRO AS.

XX PI Gaudernack G, Eriksen JA, Moller M, Gjertsen MK, Saeterdal I;
 PI Saebøe-Larsen S;

XX DR WPI; 2000-145727/13.

XX PT Protein or peptide fragments useful in the treatment and prophylaxis of
 PT cancer in mammals.

XX PS Claim 12; Page 35; 53pp; English.

XX CC This sequence represents a telomerase peptide of the invention, and can
 CC be used in a method for the treatment or prophylaxis of cancer. The
 CC sequences are useful in the treatment or prophylaxis of cancer
 CC especially, breast, lung, ovarian, cervical, colorectal, prostate or
 CC pancreatic cancers, malignant melanoma, leukaemias, lymphomas, or biliary
 CC tract carcinomas. They are useful for generating telomerase T lymphocytes
 CC capable of recognising and destroying tumour cells in a mammal,
 CC comprising culturing T lymphocytes obtained from the mammal with the
 CC peptides. Telomerase protein is expressed only by tumour cells, hence,
 CC other body cells are not targeted or destroyed by telomerase specific T
 CC cells. Note: This sequence was indexed from WO200002581, which is the
 CC first major country equivalent to NO9803141

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 43; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLVDFFLLV 9
 |||||

Db 1 RLVDFFLLV 9
 |||||

RESULT 4

AAB29462
 ID AAB29462 standard; peptide; 9 AA.

XX AC AAB29462;

XX DT 09-FEB-2001 (first entry)

XX DE HLA-A2-associated peptide BPI-190.

XX

KW Telomerase antigen variant; HLA-A2-binding; class I MHC;
 KW human leukocyte antigen; major histocompatibility complex;
 KW cytotoxic T-cell response; antigen-presenting cell; APC;
 KW telomerase-expressing cell; cancer; anticancer vaccine.
 XX
 OS Synthetic.
 XX WO200061766-A2.
 PN
 FN
 PD 19-OCT-2000.
 XX
 XX 07-APR-2000; 2000WO-IB000610.
 PF
 XX 09-APR-1999; 99US-0128539P.
 PR
 XX (BIOM-) BIOMIRA INC.
 PA
 XX Agrawal B, Longenecker BM;
 PI
 XX WPI; 2000-679493/66.
 DR
 XX New telomerase-specific T-cell antigens useful for generating T-cell
 XX responses against telomerases and for producing vaccines for treating or
 PT preventing cancer by in vivo or ex vivo techniques.
 PT
 XX Example 1; Page 22; 34pp; English.
 PS
 XX The invention relates to a human telomerase peptide antigen (AAB29461)
 CC which binds to a class I HLA (human leukocyte antigen, MHC, major
 CC histocompatibility complex), and to conservatively substituted variants
 CC thereof. The invention also relates to a vaccine comprising a telomerase
 CC antigen or antigen variant, a nucleotide encoding a telomerase antigen or
 CC variant, and a method of producing telomerase-primed antigen- presenting
 CC cell (APC) comprising contacting an APC with a composition containing a
 CC telomerase antigen or variant. The telomerase antigens or vaccine
 CC compositions are useful for inducing a cytotoxic T-cell immune response
 CC against telomerase and hence against telomerase-expressing cells (i.e.,
 CC cancer cells. Additionally, the telomerase antigen-primed APC may be
 CC coadministered with interleukin-2 for cancer treatment or prevention. The
 CC present sequence represents a peptide used in the exemplification of the
 CC invention in an assay of the cytotoxic activity of T-cells
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 100.0%; Score 43; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RLVDDFLV 9
 DB |||||
 1 RLVDDFLV 9
 RESULT 5
 AAU07432
 ID AAU07432 standard; peptide; 9 AA.
 XX
 AC AAU07432;
 XX
 XX 18-DEC-2001 (first entry)
 DT
 XX Telomerase-derived peptide #1.
 DE
 XX MUC-1; mucin; cytostatic; virucide; vaccine; adjuvant peptide; antigen;
 KW immune response; cancer; viral disease; telomerase.
 KW
 XX Synthetic.
 OS
 XX WO200170265-A2.
 PN
 XX 27-SEP-2001.
 PD
 XX 23-MAR-2001; 2001WO-IB000703.
 PF

XX 24-MAR-2000; 2000US-0191736P.
 PR (BIOM-) BIOMIRA INC.
 PA
 XX Agrawal B, Longenecker MB, Parker J;
 PI
 XX WPI; 2001-611447/70.
 DR
 XX Novel vaccine for treating and preventing disorders such as cancer and
 PT viral diseases, comprises mucin MUC-1-based adjuvant peptide and an
 PT antigen.
 XX
 XX Example 2; Page 14; 22pp; English.
 PS
 XX The invention relates to a vaccine composition comprising a mucin MUC-1-
 CC based adjuvant peptide and an antigen. The vaccine composition is useful
 CC for stimulating the immune response of a patient, by administering the
 CC vaccine. Alternatively, this can be done by contacting ex vivo a T-cell
 CC from the patient with the vaccine and administering the contacted cells
 CC to the patient which stimulates the immune system of the patient. The
 CC vaccine is useful for treating and preventing disorders such as cancer
 CC and viral diseases. The vaccine is effective in generating an immune
 CC response to an antigen against which the patient does not respond. The
 CC present sequence represents the amino acid sequence of telomerase-
 CC derived peptide #1 which was used to determine antigen promiscuity of the
 CC vaccine composition
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 100.0%; Score 43; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RLVDDFLV 9
 DB |||||
 1 RLVDDFLV 9
 RESULT 6
 AAB82773
 ID AAB82773 standard; protein; 9 AA.
 XX
 AC AAB82773;
 XX
 XX 29-OCT-2001 (first entry)
 DT
 XX Human telomerase reverse transcriptase peptide p865.
 DE
 XX Telomerase reverse transcriptase; hTERT; human; cancer; tumour;
 KW cytotoxic T lymphocyte; major histocompatibility complex;
 KW human leukocyte antigen; HLA-A2.1; vaccine.
 KW
 XX Homo sapiens.
 OS
 XX WO200160391-A1.
 PN
 XX 23-AUG-2001.
 PD
 XX 15-FEB-2001; 2001WO-US005143.
 PF
 XX 15-FEB-2000; 2000US-0182685P.
 PR
 XX 15-FEB-2001; 2001US-00182685.
 PR
 XX (REGC) UNIV CALIFORNIA.
 PA
 XX Zanetti M;
 PI
 XX WPI; 2001-536552/59.
 DR
 XX Vaccine for initiating and enhancing a cytotoxic T lymphocyte response,
 PT for treating cancers or tumors or for inducing immune response against
 PT tumors, comprises a telomerase reverse transcriptase peptide.

XX PS Example 1; Page 12; 52pp; English.

XX CC The present sequence is that of human telomerase reverse transcriptase

CC CC (hTERT) peptide p865, comprising a human leukocyte antigen HLA-A2.1

CC CC molecule binding motif corresponding to amino acid residues 865-873 of

CC CC hTERT (see AAB827765). Analysis showed that the majority of healthy

CC CC individuals as well as patients with prostate cancer immunised in vitro

CC CC against p865 or p540 (see AAB82772) developed hTERT-specific cytotoxic T

CC CC lymphocytes (CTL). The cancer patients' CTL specifically lysed a variety

CC CC of HLA-A2+ cancer cell lines such as prostate, breast, colon, lung and

CC CC melanoma, demonstrating immunological recognition of endogenously

CC CC processed hTERT peptides. In vivo immunisation of HLA-A2.1 transgenic mice

CC CC generated a specific CTL response against both hTERT peptides. The

CC CC induction of CTL responses in vitro and in vivo, and the susceptibility

CC CC to lysis of tumour cells of various origins by hTERT CTL suggest that hTERT

CC CC could serve as a universal cancer vaccine for humans. Thus, a claimed

CC CC universal vaccine for treating tumours of any origin comprises at least 1

CC CC hTERT peptide in an amount effective for initiating and enhancing a CTL

CC CC response against cancer cells. The peptide is 7-15 amino acid residues in

CC CC length and may be modified to enhance binding to the major

CC CC histocompatibility complex. Also claimed is a method for inducing and

CC CC enhancing a CTL response against cancer cells, involving harvesting blood

CC CC leucocytes, pulsing with hTERT, and contacting cancer cells with the

CC CC pulsed leucocytes. A method for targeting CTL to tumour cells is also

CC CC claimed, and involves administering a hTERT peptide to a mammal,

CC CC especially a cancer patient

XX CC Sequence 9 AA;

Query Match 100.0%; Score 43; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLVDFFLLV 9
| | | | | | | |
Db 1 RLVDFFLLV 9

RESULT 7
ABG79086
ID ABG79086 standard; peptide; 9 AA.

XX AC ABG79086;

XX DT 15-NOV-2002 (first entry)

XX DE Human HTRT class I HLA widely expressed antigen peptide #2.

XX KW Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen;
KW lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia;
KW Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
KW kidney cancer; adenocarcinoma; breast cancer; prostate cancer;
KW ovarian cancer; pancreatic cancer; epitope; vaccine; dendritic cell;
KW tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
KW cytostatic; human.

XX OS Homo sapiens.

XX FN WO200264057-A2.

XX PD 22-AUG-2002.

XX PF 15-FEB-2002; 2002WO-US005212.

XX PR 15-FEB-2001; 2001US-026867P.

XX PA (BAYU) BAYLOR COLLEGE MEDICINE.

XX PI Wang R;

XX DR WPI; 2002-627577/67.

XX

PT Novel composition for treating a disease in an animal, comprises an
PT immune effector cell and cell penetrating peptide associated with an
PT antigen or antibody.

XX PS Disclosure; Page 18; 61pp; English.

XX CC The invention relates to a composition (I) comprising an immune effector
CC cell and a cell penetrating peptide (CPP) associated with an antigen or
CC antibody. Also included are (1) a vaccine comprising (I), CPP associated
CC with an antigen, and a pharmaceutically acceptable carrier and (2)
CC preparing a composition for a disease, by providing (I) and CPP
CC associated with an antigen for disease, and introducing the antigen-
CC associated CPP to (I), where antigen enters into the cell. The antigens
CC are, for example, tumour antigen derived epitopes recognised by tumour
CC infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I
CC or II. The composition is useful for enhancing immunity in an animal to a
CC disease, by administering a mature dendritic cell comprising CPP
CC associated with an antigen to disease, to the animal, such that following
CC the administration, animal is protected from disease, where the animal
CC comprises both CD4+ and CD8+ T cells. It is also useful for treating a
CC disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung
CC cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma,
CC breast cancer, prostate cancer, ovarian cancer and pancreatic cancer).
CC The animal is further subjected to a cancer treatment including surgery,
CC radiation, chemotherapy or gene therapy. The administration of (I),
CC preferably dendritic cell is prior to, subsequent to or concurrent with,
CC the cancer treatment. The present sequence is a tumour antigen derived
CC epitope for inclusion in the composition of the invention

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 43; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLVDFFLLV 9
| | | | | | | |
Db 1 RLVDFFLLV 9

RESULT 8

AAE26819
ID AAE26819 standard; peptide; 9 AA.

XX AC AAE26819;

XX DT 13-DEC-2002 (first entry)

XX DE Human HLA-A2.1 restricted telomerase peptide epitope #1.

XX KW Human; cancer; breast cancer; ovarian cancer; melanoma; cell therapy;
KW epitope; human leukocyte antigen; HLA-A2.1.

XX OS Homo sapiens.

XX FN WO200265992-A2.

XX PD 29-AUG-2002.

XX PF 19-FEB-2002; 2002WO-US005748.

XX PR 20-FEB-2001; 2001US-0270252P.

XX PA (ORTH) ORTHO-MCNEIL PHARM INC.

XX PI Degraw J, Moriarty A, Leturcq DJ, Jackson MR, Peterson PA;

XX PI Heiskala M;

XX DR WPI; 2002-667033/71.

XX PT Treating a subject with cancer comprises combining the CD+8 cells, which
PT are stimulated with non-naturally occurring antigen-presenting cell line,

PT with adherent blood monocytes and inoculating the subject with CD8+
 PT suspension.
 XX
 PS Example 2; Page 97; 99pp; English.
 XX
 CC The invention relates to a method of treating a subject with cancer. The
 CC method involves combining the CD8+ cells, which are stimulated with non
 CC naturally occurring antigen-presenting cell (nAPC) line, with adherent
 CC blood monocytes and inoculating the subject with CD8+ suspension. The
 CC method is useful for treating cancer e.g. ovarian cancer, breast cancer
 CC and melanoma etc. It is also useful in cell therapy. The present sequence
 CC is human leukocyte antigen A2 (HLA-A2).1 restricted peptide epitope used
 CC to treat breast and ovarian cancer
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 43; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RLVDVDFLLV 9
 DB 1 RLVDVDFLLV 9
 RESULT 9
 AAEL17299
 ID AAEL17299 standard; peptide; 9 AA.
 AC AAEL17299;
 XX
 DT 18-APR-2002 (first entry)
 DE Human leukocyte antigen (HLA-A2.1) restricted peptide, P865.
 XX
 KW Human; artificial antigen presenting cell; AAPC; beta2-microglobulin;
 KW human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KW cytotoxic T lymphocyte; CTL; T cell-specific antigen; TCA; antitumour;
 KW immune response; cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200194944-A2.
 XX
 PD 13-DEC-2001.
 XX
 PF 01-JUN-2001; 2001WO-US017981.
 XX
 PR 02-JUN-2000; 2000US-0209157P.
 XX
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 XX
 PI Sadelain M, Latouche J;
 XX
 DR WPI; 2002-139667/18.
 XX
 PT Artificial antigen presenting cells for activating T lymphocytes,
 PT comprises eukaryotic cell expressing antigen presenting complex having
 PT beta2-microglobulin, exogenous accessory molecule, human leukocyte
 PT antigen molecule and protein.
 XX
 PS Example 17; Page 41; 75pp; English.
 XX
 CC The present invention relates to an artificial antigen presenting cell
 CC (AAPC) comprising a eukaryotic cell expressing an antigen presenting
 CC complex comprising beta2-microglobulin, an exogenous accessory molecule,
 CC a human leukocyte antigen, HLA (major histocompatibility complex, MHC),
 CC molecule of a single type and a protein that is processed intracellularly
 CC to produce an exogenous T cell-specific epitope. The invention also
 CC relates to methods for activation of T lymphocytes. The method is also
 CC useful for identifying within a test population of cytotoxic T
 CC lymphocytes (CTLs) CTLs specifically activated against a known T-cell
 CC specific antigen (TCA), which is useful for diagnostic purposes. AAPC is

CC also useful for activating CTLs, by contacting AAPC with a suitable
 CC population of T lymphocytes under conditions suitable for the activation
 CC and isolating the activated CTLs. AAPC is further useful for the
 CC investigation of primary T cell activation and diagnostic applications
 CC here primary T cell activation allow discovery of antigens and accessory
 CC molecules, and diagnostic applications include cell-based assays for
 CC quantifying immune response in normal, infected or treated (vaccinated)
 CC patients. Composition comprising AAPC or activated T cells produced by
 CC utilising AAPC is useful for eliciting an antitumour response. The
 CC invention is used for the treatment of cancer. The present sequence is
 CC human HLA-A2.1 restricted peptide used in additional AAPC-induced CTL-
 CC activation
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 43; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RLVDVDFLLV 9
 DB 1 RLVDVDFLLV 9
 RESULT 10
 ADA89162
 ID ADA89162 standard; peptide; 9 AA.
 XX
 AC ADA89162;
 XX
 DT 20-NOV-2003 (first entry)
 DE hTERT derived peptide T865 SEQ ID NO:6.
 XX
 KW immunoglobulin; Ig; heavy chain variable domain;
 KW light chain variable domain; major histocompatibility complex; MHC;
 KW gp100; MUC1; TAX; hTERT; cytostatic; gene therapy; cancerous disorder;
 KW cancer.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO2003070752-A2.
 XX
 PD 28-AUG-2003.
 XX
 PF 20-FEB-2003; 2003WO-US005128.
 XX
 PR 20-FEB-2002; 2002US-0358994P.
 XX
 PA (DYAX-) DYAX CORP.
 PA (TECR) TECHNION RES & DEV FOUND LTD.
 XX
 PI Hoogenboom HRJM, Reiter Y;
 XX
 DR WPI; 2003-663847/62.
 XX
 PT New protein comprising an immunoglobulin heavy chain variable (VH) domain
 PT and an immunoglobulin light chain variable (VL) domain, useful for
 PT preparing a composition for treating or preventing a cancerous disorder.
 XX
 PS Claim 3; Page 137; 224pp; English.
 XX
 CC The present invention describes a protein comprising an immunoglobulin
 CC (Ig) heavy chain variable (VH) domain and an Ig light chain variable (VL)
 CC domain. The protein binds a complex comprising a major histocompatibility
 CC complex (MHC) and a peptide, does not substantially bind the MHC in the
 CC absence of the bound peptide, and does not substantially bind the peptide
 CC in the absence of the MHC. The peptide is a peptide fragment of gp100,
 CC MUC1, TAX or hTERT. Also described: (1) a pharmaceutical composition
 CC comprising the novel protein and a carrier; (2) a cytotoxic T cell
 CC comprising one or more nucleic acids for expressing the Ig that binds a
 CC complex having an MHC and a peptide, does not substantially bind the MHC

CC in the absence of the bound peptide, and does not substantially bind the
 CC peptide in the absence of the MHC; (3) an isolated nucleic acid
 CC comprising a first segment that encodes the Ig variable domain; (4) a
 CC host cell comprising heterologous nucleic acid sequences that encodes the
 CC novel protein; (5) a transgenic animal whose genome includes heterologous
 CC nucleic acid sequences that encode the protein; (6) identifying the
 CC protein that specifically binds the MHC-peptide complex; (7) expressing
 CC an antigen-binding protein; (8) ablating or killing a target cell that
 CC displays a peptide on a surface MHC molecule; (9) treating or preventing
 CC a cancerous disorder in a subject; and (10) detecting an MHC-peptide
 CC complex in a sample. A protein of the invention has cytostatic activity,
 CC and can be used in gene therapy. The protein is useful for preparing a
 CC composition for treating or preventing a cancerous disorder. The present
 CC sequence represents a hTERT-derived peptide, which is used in the
 CC exemplification of the present invention.

XX Sequence 9 AA;

Query Match 100.0%; Score 43; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLVDDEFLV 9
 Db 1 RLVDDEFLV 9

RESULT 11

AAE38656
 ID AAE38656 standard; peptide; 9 AA.

XX
 AC AAE38656;

XX 04-DEC-2003 (first entry)

XX HLA-A2 restricted peptide, hTERT (865).

XX Major histocompatibility complex; MHC; HLA-restricted antigen; cancer;
 KW viral infection; autoimmune disease; gene therapy; cytostatic; virucide;
 KW immunomodulator.

XX Unidentified.

XX WO2003068201-A2.

XX 21-AUG-2003.

XX 11-FEB-2003; 2003WO-IL000105.

XX 13-FEB-2002; 2002US-00073301.

XX (TECR) TECHNION RES & DEV FOUND LTD.

XX Reiter Y, Denberg G;

XX WPI; 2003-689603/65.

PT New isolated molecule comprising an antibody that binds with a human
 PT major histocompatibility complex (MHC) class I being complexed with a HLA
 PT -restricted antigen, useful for treating cancer, viral infection or
 PT autoimmune disease.

XX Example; Page 10; 81pp; English.

XX The invention relates to an isolated molecule comprising an antibody
 CC specifically bindable with a binding affinity below 20 nanomolar to a
 CC human major histocompatibility complex (MHC) class I being complexed with
 CC HLA-restricted antigen. The molecules, antibodies, and methods are
 CC useful for treating cancer, viral infection and an autoimmune disease.
 CC The invention is useful in gene therapy. The present sequence is HLA-A2
 CC restricted peptide

XX Sequence 9 AA;

Query Match 100.0%; Score 43; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLVDDEFLV 9
 Db 1 RLVDDEFLV 9

RESULT 12

ADG89652
 ID ADG89652 standard; peptide; 9 AA.

XX
 AC ADG89652;

XX 11-MAR-2004 (first entry)

XX Class I HLA-restricted widely expressed antigen #17.
 KW metastatic cancer cell differentiation; mutated fibronectin;
 KW metastatic cancer; class I HLA-restricted; widely antigen.

XX Unidentified.

XX WO2003100027-A2.

XX 04-DEC-2003.

XX 28-MAY-2003; 2003WO-US016736.

XX 28-MAY-2002; 2002US-0383530P.

XX (BAYU) BAYLOR COLLEGE MEDICINE.

XX Wang R;

XX WPI; 2004-035134/03.

PT Identifying a cell that differentiates into a metastatic cancer cell,
 PT useful for preventing metastatic cancer, comprises identifying a mutated
 PT fibronectin in the cell.

XX Disclosure; SEQ ID NO 95; 137pp; English.

XX The invention comprises a method for identifying a cell that will
 CC differentiate into a metastatic cancer cell, the method involves
 CC identifying a mutated fibronectin in the cell. The method of the
 CC invention is useful for preventing metastatic cancer. The present amino
 CC acid sequence represents a Class I HLA-restricted widely expressed
 CC antigen.

XX Sequence 9 AA;

Query Match 100.0%; Score 43; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLVDDEFLV 9
 Db 1 RLVDDEFLV 9

RESULT 13

ADS52358
 ID ADS52358 standard; peptide; 9 AA.

XX
 AC ADS52358;

XX 16-DEC-2004 (first entry)

XX HLA-A2 restricted peptide from hTERT #2.

XX

KW Antibody; Fab; HLA-A2; Tax 11-19; human leukocyte antigen; antigen;
KW T lymphocyte; antigen-presenting cell; B cell; dendritic cell;
KW major histocompatibility complex; MHC class I; viral infection;
KW human T lymphotropic virus-1 infection; viral oncoprotein;
KW mycoplasma infection; bacterial infection; fungal infection;
KW protozoal infection; phase display.
XX
XX
OS Unidentified.
XX
XX US2004191260-A1.
XX
XX 30-SEP-2004.
XX
XX 26-MAR-2003; 2003US-00396578.
XX
XX 26-MAR-2003; 2003US-00396578.
XX
XX (TECR) TECHNION RES & DEV FOUND LTD.
XX
XX Reiter Y, Cohen C;
XX
XX WPI; 2004-735863/72.
XX
XX New composition comprising a multimeric form of an antibody or fragment
XX which specifically binds an antigen-presenting portion of a complex,
XX useful for treating pathogen-associated diseases e.g., HIV.
XX
XX Example 1; SEQ ID NO 9; 68pp; English.
XX
XX The invention relates to a composition-of-matter comprising (a multimeric
XX form of) an antibody or antibody fragment including an antigen-binding
XX region capable of specifically binding an antigen-presenting portion of a
XX complex composed of a human antigen-presenting molecule and an antigen
XX derived from a pathogen. Also included are an isolated polynucleotide
XX comprising a nucleic acid sequence encoding an antibody fragment (the
XX antibody fragment including an antigen-binding region capable of
XX specifically binding an antigen-presenting portion of a complex composed
XX of a human antigen-presenting molecule and an antigen derived from a
XX pathogen), a nucleic acid construct comprising the isolated
XX polynucleotide above (and a promoter sequence for directing transcription
XX of the isolated polynucleotide in a host cell), a host cell comprising
XX the nucleic acid construct above, a host virus comprising the nucleic
XX acid construct above, a virus comprising a coat protein fused to the
XX antibody fragment, detecting an antigen-presenting portion of a complex
XX composed of a human antigen-presenting molecule and an antigen derived
XX from a pathogen, a method of diagnosing an infection by a pathogen in an
XX individual, a method of killing or damaging a target cell
XX expressing/displaying an antigen-presenting portion of a complex
XX (composed of a human antigen-presenting molecule and an antigen derived
XX from a pathogen) and a method of detecting in a biological sample an
XX antigen-presenting portion of a complex as described above. The target
XX cell is a T lymphocyte or an antigen-presenting cell, which is a B cell
XX or a dendritic cell. The composition-of-matter further comprises a
XX detectable moiety attached to the antibody or antibody fragment. The
XX detectable moiety is a recognition sequence of a biotin protein ligase, a
XX biotin molecule, a streptavidin molecule, a fluorophore, an enzyme or a
XX polystyrene tag. The biotin protein ligase is BirA, the fluorophore is
XX phycoerythrin, and the enzyme is horseradish peroxidase. The toxin is
XX pseudomonas exotoxin A or its portion, which is a translocation domain
XX of an ADP ribosylation domain. The human antigen-presenting molecule
XX is a major histocompatibility complex (MHC), preferably MHC class I
XX molecule, more preferably HLA-A2 molecule. The pathogen is viral,
XX preferably a retrovirus, more preferably human T lymphotropic virus-1.
XX The antigen derived from a pathogen is restricted by the antigen-
XX presenting molecule and is a polypeptide selected from a segment of a
XX viral oncoprotein or a segment of a Tax protein. A pharmaceutical
XX composition comprising an active ingredient the composition-of-matter
XX is useful in a method for treating a disease associated with a pathogen
XX in an individual such as viruses (HIV), mycoplasmas, bacteria, fungi and
XX protozoans. The composition-of-matter or the methods are useful for
XX diagnosing an infection by a pathogen in an individual and for killing or
XX damaging a target cell expressing or displaying an antigen-presenting
XX portion of a complex composed of a human antigen-presenting molecule and

CC an antigen derived from a pathogen. A phage displayed library of human
CC Fab antibodies which recognise an HLA-A2/Tax 11-19 complex was generated
CC and tested for specific binding to HLA-A2/Tax 11-19, individual clones
CC were then sequenced and their CDR (complementarity determining region)
CC sequences compared. The present sequence is a HLA-A2 restricted negative
CC control peptide.
XX
XX Sequence 9 AA;
SQ
Query Match 100.0%; Score 43; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 RLVDDELLV 9
| | | | | | | | | |
Db 1 RLVDDELLV 9
| | | | | | | | | |
RESULT 14
AAY96397
ID AAY96397 standard; peptide; 10 AA.
XX
XX AC AAY96397;
XX
XX DT 29-AUG-2000 (first entry)
XX
XX DE HLA-A2 binding peptide hTERT R865.
XX
XX KW hTERT; telomerase complex; reverse transcriptase; MHC; HLA; CTL; cancer;
XX KW human leukocyte antigen; tumour-associated antigen; cytostatic; vaccine;
XX KW major histocompatibility complex; cytotoxic T lymphocyte; immunotherapy.
XX
XX OS Homo sapiens.
XX
XX PN WO200025813-A1.
XX
XX PD 11-MAY-2000.
XX
XX PF 29-OCT-1999; 99WO-US025438.
XX
XX PR 29-OCT-1998; 98US-0106106P.
XX
XX PA (DAND) DANA FARRER CANCER INST INC.
XX PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX
XX PI Nadler LM, Hahn WC, Schultze JL, Vonderheide RH;
XX WPI; 2000-365402/31.
XX
XX Universal tumor-associated antigens such as telomerase catalytic subunit
XX capable of binding major histocompatibility complex molecule useful for
XX diagnosis, prevention and treatment of cancer.
XX
XX Disclosure; Page 76; 136pp; English.
XX
XX Human telomerase complex reverse transcriptase (hTERT) is expressed in
XX more than 85 percent of human cancers. hTERT is useful as a universal
XX tumour-associated antigen (TAA) that binds to a major histocompatibility
XX complex molecule (MHC). hTERT peptides were analyzed for the ability to
XX bind to HLA (human leukocyte antigen) class I molecules. Cytotoxic T
XX lymphocytes (CTL) were then generated that kill a cell expressing hTERT
XX or a hTERT-TAA, in a hTERT or TAA specific MHC-restricted fashion.
XX Antigen presenting cells (APC) were also generated ex vivo for
XX presentation of a TAA peptide or hTERT. The APC can be used to activate
XX CTL to kill cells expressing the TAA. The TAA, hTERT peptides, APC and
XX CTL are useful for cancer immunotherapy. Measuring the level of CTL in a
XX sample is useful for assessing the level of immunity of a patient to a
XX TAA or a peptide, where the sample is obtained before or after a cancer
XX treatment is given to the patient. TAA peptides (e.g. hTERT) are also
XX useful for diagnosis and prophylactic treatment of cancer
XX
XX Sequence 10 AA;

Query Match 100.0%; Score 43; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLVDDFLLV 9
| | | | | | | |
Db 1 RLVDDFLLV 9

RESULT 15

AAV86591
ID AAY86591 standard; peptide; 13 AA.

XX AC AAY86591;

XX DT 05-MAY-2000 (first entry)

XX DE Telomerase peptide #6.

XX KW Telomerase; antigenic peptide; cancer; therapy; human; tumour cell;
KW malignant melanoma; leukaemia; lymphoma; biliary tract carcinoma;
KW telomerase T lymphocyte.

XX OS Homo sapiens.

XX PN WO200002581-A1.

XX PD 20-JAN-2000.

XX PF 30-JUN-1999; 99WO-NO000220.

XX PR 08-JUL-1998; 98NO-00003141.

XX PA (NHVD) NORSK HYDRO AS.

XX PI Gaudernack G, Eriksen JA, Moller M, Gjertsen MK, Saeterdal I;

XX PI Saeboe-Larsen S;

XX DR WPI; 2000-145727/13.

XX PT Protein or peptide fragments useful in the treatment and prophylaxis of
PT cancer in mammals.

XX PS Claim 9; Page 34; 53pp; English.

XX CC This sequence represents a telomerase peptide of the invention, and can
CC be used in a method for the treatment or prophylaxis of cancer. The
CC sequences are useful in the treatment or prophylaxis of cancer.
CC especially, breast, lung, ovarian, cervical, colorectal, prostate or
CC pancreatic cancers, malignant melanoma, leukaemias, lymphomas, or biliary
CC tract carcinomas. They are useful for generating telomerase T lymphocytes
CC capable of recognising and destroying tumour cells in a mammal.
CC comprising culturing T lymphocytes obtained from the mammal with the
CC peptides. Telomerase protein is expressed only by tumour cells, hence,
CC other body cells are not targeted or destroyed by telomerase specific T
CC cells. Note: This sequence was indexed from WO200002581, which is the
CC first major country equivalent to NO9803141

SQ Sequence 13 AA;

Query Match 100.0%; Score 43; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLVDDFLLV 9
| | | | | | | |
Db 4 RLVDDFLLV 12

Search completed: May 4, 2005, 12:24:15
Job time : 122.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 4, 2005, 12:20:14 ; Search time 30 Seconds
(without alignments)
22.395 Million cell updates/sec

Title: US-09-788-110A-1

Perfect score: 50

Sequence: 1 ILAKFLHWL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	364	4	US-09-417-485D-40
2	50	100.0	437	4	US-09-582-924B-2
3	50	100.0	438	4	US-09-582-924B-10
4	50	100.0	514	3	US-08-974-549A-605
5	50	100.0	514	4	US-08-912-951-319
6	50	100.0	514	4	US-09-402-181B-605
7	50	100.0	514	4	US-09-721-456-605
8	50	100.0	622	4	US-09-582-924B-12
9	50	100.0	807	3	US-08-974-549A-5
10	50	100.0	807	4	US-08-912-951-5
11	50	100.0	807	4	US-09-402-181B-5
12	50	100.0	807	4	US-09-721-456-5
13	50	100.0	1003	3	US-08-851-843A-217
14	50	100.0	1003	3	US-08-974-549A-336
15	50	100.0	1003	3	US-08-854-050-217
16	50	100.0	1003	3	US-09-430-323-217
17	50	100.0	1003	3	US-08-402-181B-336
18	50	100.0	1003	4	US-09-721-456-336
19	50	100.0	1132	3	US-08-851-843A-225
20	50	100.0	1132	3	US-08-974-549A-2
21	50	100.0	1132	3	US-08-974-549A-344
22	50	100.0	1132	3	US-08-854-050-225
23	50	100.0	1132	3	US-09-430-323-225
24	50	100.0	1132	3	US-09-128-354-2
25	50	100.0	1132	4	US-09-675-321-2
26	50	100.0	1132	4	US-09-052-919-2
27	50	100.0	1132	4	US-08-912-951-2

28 50 100.0 1132 4 US-09-402-181B-2 Sequence 2, Appli
29 50 100.0 1132 4 US-09-402-181B-344 Sequence 344, App
30 50 100.0 1132 4 US-09-721-456-2 Sequence 2, Appli
31 50 100.0 1132 4 US-09-721-456-344 Sequence 344, App
32 50 100.0 1132 4 US-09-953-052-2 Sequence 2, Appli
33 50 100.0 1132 4 US-09-042-460-3 Sequence 3, Appli
34 50 100.0 1132 4 US-09-949-016-6326 Sequence 6326, Ap
35 50 100.0 1154 3 US-08-974-549A-611 Sequence 611, App
36 50 100.0 1154 4 US-08-912-951-323 Sequence 323, App
37 50 100.0 1154 4 US-09-402-181B-611 Sequence 611, App
38 50 100.0 1154 4 US-09-721-456-611 Sequence 611, App
39 50 100.0 1189 3 US-08-974-549A-613 Sequence 613, App
40 50 100.0 1189 4 US-08-912-951-325 Sequence 325, App
41 50 100.0 1189 4 US-09-402-181B-613 Sequence 613, App
42 50 100.0 1189 4 US-09-721-456-613 Sequence 613, App
43 50 100.0 1193 4 US-09-949-016-11712 Sequence 11712, A
44 50 100.0 1200 3 US-08-974-549A-612 Sequence 612, App
45 50 100.0 1200 4 US-08-912-951-324 Sequence 324, App

ALIGNMENTS

RESULT 1

US-09-417-485D-40
; Sequence 40, Application US/09417485D
; Patent No. 6541202
; GENERAL INFORMATION:
; APPLICANT: Long, David M.
; APPLICANT: Metz, Anneke M.
; APPLICANT: Love, Ruschelle A.
; TITLE OF INVENTION: Telomerase Reverse Transcriptase (TERT) Genes
; FILE REFERENCE: 47714-5009-US
; CURRENT APPLICATION NUMBER: US/09/417.485D
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Partial TERT sequence
US-09-417-485D-40

Query Match 100.0%; Score 50; DB 4; Length 364;

Best Local Similarity 100.0%; Pred. No. 1.3;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILAKFLHWL 9
Db 77 ILAKFLHWL 85

RESULT 2

US-09-582-924B-2
; Sequence 2, Application US/09582924B
; Patent No. 6608188
; GENERAL INFORMATION:
; APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA
; TITLE OF INVENTION: No. 6608188el Gene Having Reverse Transcriptase Motif
; FILE REFERENCE: 46124-5034-US
; CURRENT APPLICATION NUMBER: US/09/582.924B
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: JP 10/13232
; PRIOR FILING DATE: 1998-01-08
; PRIOR APPLICATION NUMBER: JP 10/33584
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: JP 10/139177
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: PCT/JP99/00039
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 13

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; SEQ ID NO 2
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION:
US-09-582-924B-2

Query Match      100.0%; Score 50; DB 4; Length 437;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILAKFLHWL 9
Db 30 ILAKFLHWL 38

RESULT 3
US-09-582-924B-10
; Sequence 10, Application US/09582924B
; Patent No. 6608188
; GENERAL INFORMATION:
; APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA
; TITLE OF INVENTION: No. 6608188e1 Gene Having Reverse Transcriptase Motif
; FILE REFERENCE: 46124-5034-US
; CURRENT APPLICATION NUMBER: US/09/582,924B
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: JP 10/13232
; PRIOR FILING DATE: 1998-01-08
; PRIOR APPLICATION NUMBER: JP 10/33584
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: JP 10/139177
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: PCT/JP99/00039
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 10
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION:
US-09-582-924B-10

Query Match      100.0%; Score 50; DB 4; Length 438;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILAKFLHWL 9
Db 30 ILAKFLHWL 38

RESULT 4
US-08-974-549A-605
; Sequence 605, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA

; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 605:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 514 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..515
; OTHER INFORMATION: /note= "fusion protein composed of
; OTHER INFORMATION: glutathione-S-transferase sequence,
; OTHER INFORMATION: thrombin cleavage sequence, recognition
; OTHER INFORMATION: sequence for heart muscle protein
; OTHER INFORMATION: kinase, residues introduced by cloning
; OTHER INFORMATION: and hTERT protein fragment"
US-08-974-549A-605

Query Match      100.0%; Score 50; DB 3; Length 514;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILAKFLHWL 9
Db 495 ILAKFLHWL 503
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RESULT 5
US-08-912-951-319
; Sequence 319, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; TITLE OF INVENTION: THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,951
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 319:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 514 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-912-951-319

Query Match 100.0%; Score 50; DB 4; Length 514;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
US-09-402-181B-605
; Sequence 605, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181B
; FILING DATE: 29-Sep-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ausehus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-002620US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 605:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 514 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..515
; OTHER INFORMATION: /note="fusion protein composed of
; glutathione-S-transferase sequence,
; thrombin cleavage sequence, recognition

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; sequence for heart muscle protein
; kinase, residues introduced by cloning
; and hTERT protein fragment"
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 605:
US-09-402-181B-605

Query Match      100.0%; Score 50; DB 4; Length 514;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ILAKFLHML 9
Db      495 ILAKFLHML 503

RESULT 7
US-09-721-456-605
; Sequence 605, Application US/09721456
; Patent No. 6617110
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
;
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/721,456
; FILING DATE: 22-NOV-2000
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-00261005
; TELECOMMUNICATION INFORMATION:

;
; sequence for heart muscle protein
; kinase, residues introduced by cloning
; and hTERT protein fragment"
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 605:
US-09-402-181B-605

Query Match      100.0%; Score 50; DB 4; Length 514;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ILAKFLHML 9
Db      495 ILAKFLHML 503

RESULT 8
US-09-582-924B-12
; Sequence 12, Application US/09582924B
; Patent No. 6608188
; GENERAL INFORMATION:
; APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA
; TITLE OF INVENTION: No. 6608188ei Gene Having Reverse Transcriptase Motif
; FILE REFERENCE: 46124-5034-US
; CURRENT APPLICATION NUMBER: US/09/582,924B
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: JP 10/13232
; PRIOR FILING DATE: 1998-01-08
; PRIOR APPLICATION NUMBER: JP 10/33584
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: JP 10/139177
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: PCT/JP99/00039
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 12
; LENGTH: 622
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION:
US-09-582-924B-12

Query Match      100.0%; Score 50; DB 4; Length 622;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ILAKFLHML 9
Db      30 ILAKFLHML 38

RESULT 9
US-08-974-549A-5
; Sequence 5, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
```

APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 807 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-974-549A-5

Query Match 100.0%; Score 50; DB 3; Length 807;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILAKFLHWL 9

Db 540 ILAKFLHWL 548

RESULT 10
US-08-912-951-5
Sequence 5, Application US/08912951
Patent No. 6475789
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 807 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-912-951-5

Query Match 100.0%; Score 50; DB 4; Length 807;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

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Oy      1 ILAKFLHWL 9
Db      540 ILAKFLHWL 548

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
US-09-402-181B-5
; Sequence 5, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; APPLICATION NUMBER: US/09/402,181B
; FILING DATE: 29-Sep-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ausenhus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-002620US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 807 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-402-181B-5

Query Match      100.0%; Score 50; DB 4; Length 807;
Best Local Similarity 100.0%; Pred. No. 2.5;

Oy      1 ILAKFLHWL 9
Db      540 ILAKFLHWL 548

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 5, Application US/09721456
; Patent No. 6617110
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/721,456
; FILING DATE: 22-No. 6617110-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 807 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-721-456-5

Query Match 100.0%; Score 50; DB 4; Length 807;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILAKFLHWL 9
DB 540 ILAKFLHWL 548

RESULT 13

US-08-851-843A-217
; Sequence 217, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 217:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1003 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-851-843A-217

Query Match 100.0%; Score 50; DB 3; Length 1003;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILAKFLHWL 9
DB 411 ILAKFLHWL 419

RESULT 14

US-08-974-549A-336
; Sequence 336, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
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; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 336;
SEQUENCE CHARACTERISTICS:
LENGTH: 1003 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-549A-336

Query Match 100.0%; Score 50; DB 3; Length 1003;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILAKFLHWL 9
Db 411 ILAKFLHWL 419

RESULT 15

US-08-854-050-217
Sequence 217, Application US/08854050
Patent No. 6261836

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 217:
SEQUENCE CHARACTERISTICS:

LENGTH: 1003 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-854-050-217

Query Match 100.0%; Score 50; DB 3; Length 1003;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILAKFLHWL 9
Db 411 ILAKFLHWL 419

Search completed: May 4, 2005, 12:41:38
Job time : 31 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 4, 2005, 12:28:20 ; Search time 91.5 Seconds
(without alignments)
32.765 Million cell updates/sec

Title: US-09-788-110A-1

Perfect score: 50

Sequence: 1 ILAKFLHWL 9

Scoring table: BLOSUM62

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Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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2	50	100.0	9	11 US-09-788-110A-1	Sequence 1, Appl
3	50	100.0	9	13 US-10-080-013-34	Sequence 34, Appl
4	50	100.0	9	15 US-10-371-942-5	Sequence 5, Appl
5	50	100.0	9	15 US-10-447-161-93	Sequence 93, Appl
6	50	100.0	9	15 US-10-447-161-94	Sequence 94, Appl
7	50	100.0	9	15 US-10-289-566-34	Sequence 34, Appl
8	50	100.0	9	15 US-10-333-430-60	Sequence 60, Appl
9	50	100.0	9	16 US-10-396-578-8	Sequence 8, Appl
10	50	100.0	291	14 US-10-282-960-3	Sequence 3, Appl
11	50	100.0	364	14 US-10-304-095-40	Sequence 40, Appl
12	50	100.0	437	14 US-10-294-778-2	Sequence 2, Appl
13	50	100.0	438	14 US-10-294-778-10	Sequence 10, Appl

14	50	100.0	500	14	US-10-282-960-81	Sequence 81, Appl
15	50	100.0	514	14	US-10-044-692-319	Sequence 319, Appl
16	50	100.0	514	14	US-10-044-692-319	Sequence 319, Appl
17	50	100.0	514	15	US-10-325-810-605	Sequence 605, Appl
18	50	100.0	514	17	US-10-877-146-605	Sequence 605, Appl
19	50	100.0	622	14	US-10-294-778-12	Sequence 12, Appl
20	50	100.0	807	14	US-10-044-692-5	Sequence 5, Appl
21	50	100.0	807	14	US-10-044-692-5	Sequence 5, Appl
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23	50	100.0	807	17	US-10-877-146-5	Sequence 5, Appl
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25	50	100.0	1003	10	US-09-438-486-217	Sequence 217, Appl
26	50	100.0	1003	14	US-10-053-758-217	Sequence 217, Appl
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28	50	100.0	1003	14	US-10-054-611-217	Sequence 217, Appl
29	50	100.0	1003	15	US-10-325-810-336	Sequence 336, Appl
30	50	100.0	1003	17	US-10-877-146-336	Sequence 336, Appl
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32	50	100.0	1132	9	US-09-749-728B-31	Sequence 31, Appl
33	50	100.0	1132	9	US-09-843-676-325	Sequence 225, Appl
34	50	100.0	1132	9	US-09-953-052-2	Sequence 2, Appl
35	50	100.0	1132	11	US-09-788-110A-23	Sequence 23, Appl
36	50	100.0	1132	14	US-10-053-758-225	Sequence 225, Appl
37	50	100.0	1132	14	US-10-208-243-2	Sequence 2, Appl
38	50	100.0	1132	14	US-10-054-295-225	Sequence 225, Appl
39	50	100.0	1132	14	US-10-054-611-225	Sequence 225, Appl
40	50	100.0	1132	14	US-10-105-963-2	Sequence 2, Appl
41	50	100.0	1132	14	US-10-044-692-2	Sequence 2, Appl
42	50	100.0	1132	14	US-10-044-692-2	Sequence 2, Appl
43	50	100.0	1132	14	US-10-295-681-57	Sequence 57, Appl
44	50	100.0	1132	15	US-10-325-810-2	Sequence 2, Appl
45	50	100.0	1132	15	US-10-325-810-344	Sequence 344, Appl

ALIGNMENTS

RESULT 1

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US-09-815-346-11
; Sequence 11, Application US/09815346
; Publication No. US20020018806A1
; GENERAL INFORMATION:
; APPLICANT: AGRAWAL, BABITA
; APPLICANT: LONGENECKER, MICHAEL B.
; TITLE OF INVENTION: LIPOPEPTIDE ADJUVANTS
; FILE REFERENCE: 042881/0160
; CURRENT APPLICATION NUMBER: US/09/815,346
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/191,736
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Telomerase-derived
; OTHER INFORMATION: antigenic peptide
US-09-815-346-11

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Query Match 100.0%; Score 50; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILAKFLHWL 9

Db 1 ILAKFLHWL 9

RESULT 2

US-09-788-110A-1

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; Publication No. US20040086518A1
; GENERAL INFORMATION:
; APPLICANT: Zanetti, Maurizio
; TITLE OF INVENTION: A Universal Vaccine and Method for Treating Cancer Employing
; FILE REFERENCE: UCSD-07017
; CURRENT APPLICATION NUMBER: US/09/788,110A
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-110A-1

Query Match      100.0%; Score 50; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ILAKFLHWL 9
Db      1 ILAKFLHWL 9

RESULT 3
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; Sequence 34, Application US/10080013
; Publication No. US20030077248A1
; GENERAL INFORMATION:
; APPLICANT: Moriarty, Ann
; APPLICANT: Leturcq, Didier
; APPLICANT: Degraw, Juli
; APPLICANT: Heiskala, Marja
; APPLICANT: Peterson, Per
; APPLICANT: Jackson, Michael
; TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS
; FILE REFERENCE: ORT-1557
; CURRENT APPLICATION NUMBER: US/10/080,013
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-080-013-34

Query Match      100.0%; Score 50; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ILAKFLHWL 9
Db      1 ILAKFLHWL 9

RESULT 4
US-10-371-942-5
; Sequence 5, Application US/10371942
; Publication No. US20030223994A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034001
; CURRENT APPLICATION NUMBER: US/10/371,942
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,994
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0

Query Match      100.0%; Score 50; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-371-942-5

Query Match      100.0%; Score 50; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ILAKFLHWL 9
Db      1 ILAKFLHWL 9

RESULT 5
US-10-447-161-93
; Sequence 93, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 93
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-93

Query Match      100.0%; Score 50; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ILAKFLHWL 9
Db      1 ILAKFLHWL 9

RESULT 6
US-10-447-161-94
; Sequence 94, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 94
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-94

Query Match      100.0%; Score 50; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ILAKFLHWL 9
Db      1 ILAKFLHWL 9
```

Db 1 ILAKFLHWL 9
|||||

RESULT 7

US-10-289-566-34
; Sequence 34, Application US/10289566
; Publication No. US20040071671A1
; GENERAL INFORMATION:
; APPLICANT: Leturcq, Didier J.
; APPLICANT: Moriarty, Ann M.
; APPLICANT: Jackson, Michael R.
; APPLICANT: Peterson, Per A.
; APPLICANT: Richards, Jon M.
; TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS
; FILE REFERENCE: ORT 1342CIP
; CURRENT APPLICATION NUMBER: US/10/289,566
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/270,252
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: US 10/080,013
; PRIOR FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO. 34
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-289-566-34

Query Match 100.0%; Score 50; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILAKFLHWL 9
|||||

Db 1 ILAKFLHWL 9

RESULT 8

US-10-333-430-60
; Sequence 60, Application US/10333430
; Publication No. US20040072240A1
; GENERAL INFORMATION:
; APPLICANT: INSERM
; APPLICANT: INSTITUT GUSTAVE ROUSSY
; APPLICANT: KOSMATOPOULOS, Kostas
; APPLICANT: TOURDOT, Sophie
; APPLICANT: SCARDINO, Antonio
; APPLICANT: GROSS, David, Alexandre
; TITLE OF INVENTION: METHOD FOR SCREENING PEPTIDES FOR USE IN
; TITLE OF INVENTION: IMMUNOTHERAPY
; FILE REFERENCE: 33339/259034
; CURRENT APPLICATION NUMBER: US/10/333,430
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: FR 0009591
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-333-430-60

Query Match 100.0%; Score 50; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILAKFLHWL 9
|||||

Db 1 ILAKFLHWL 9

RESULT 9

US-10-396-578-8
; Sequence 8, Application US/10396578
; Publication No. US20040191260A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram J.
; APPLICANT: Cohen, Cyril J.
; TITLE OF INVENTION: COMPOSITIONS CAPABLE OF SPECIFICALLY BINDING PARTICULAR HUMAN
; TITLE OF INVENTION: ANTIGEN PRESENTING MOLECULE/PATHOGEN-DERIVED ANTIGEN COMPLEXES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 25563
; CURRENT APPLICATION NUMBER: US/10/396,578
; CURRENT FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: HLA-A2 restricted peptide
US-10-396-578-8

Query Match 100.0%; Score 50; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILAKFLHWL 9
|||||

Db 1 ILAKFLHWL 9

RESULT 10

US-10-282-960-3
; Sequence 3, Application US/10282960
; Publication No. US20030143228A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Si-Yi
; APPLICANT: ZhaoYang, You
; APPLICANT: Schroers, Roland
; TITLE OF INVENTION: Human Telomerase Reverse Transcriptase as a Class-II Restricted T
; TITLE OF INVENTION: Associated Antigen
; FILE REFERENCE: P02193US1
; CURRENT APPLICATION NUMBER: US/10/282,960
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 60/345,012
; PRIOR FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Human
US-10-282-960-3

Query Match 100.0%; Score 50; DB 14; Length 291;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILAKFLHWL 9
|||||

Db 1 ILAKFLHWL 9

RESULT 11

US-10-304-095-40
; Sequence 40, Application US/10304095
; Publication No. US20030134275A1

; GENERAL INFORMATION:
 ; APPLICANT: Long, David M.
 ; APPLICANT: Metz, Anneke M.
 ; APPLICANT: Love, Ruschellie A.
 ; TITLE OF INVENTION: Telomerase Reverse Transcriptase (TERT) Genes
 ; FILE REFERENCE: 47714-5009-US
 ; CURRENT APPLICATION NUMBER: US/10/304,095
 ; CURRENT FILING DATE: 2002-11-26
 ; PRIOR APPLICATION NUMBER: US/09/417,485
 ; PRIOR FILING DATE: 2002-06-14
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 40
 ; LENGTH: 364
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: Partial TERT sequence
 US-10-304-095-40

Query Match 100.0%; Score 50; DB 14; Length 364;
 Best Local Similarity 100.0%; Pred. No. 5.8; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;

Qy 1 ILAKFLHWL 9
 |||||
 Db 77 ILAKFLHWL 85

RESULT 12
 US-10-294-778-2
 ; Sequence 2, Application US/10294778
 ; Publication No. US20030060417A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA
 ; TITLE OF INVENTION: No. US20030060417A1el Gene Having Reverse Transcriptase Motif
 ; FILE REFERENCE: 46124-5034-US
 ; CURRENT APPLICATION NUMBER: US/10/294,778
 ; CURRENT FILING DATE: 2002-11-15
 ; PRIOR APPLICATION NUMBER: US/09/582,924
 ; PRIOR FILING DATE: 2000-07-07
 ; PRIOR APPLICATION NUMBER: JP 10/13232
 ; PRIOR FILING DATE: 1998-01-08
 ; PRIOR APPLICATION NUMBER: JP 10/33584
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: JP 10/139177
 ; PRIOR FILING DATE: 1998-05-06
 ; PRIOR APPLICATION NUMBER: PCT/JP99/00039
 ; PRIOR FILING DATE: 1999-01-08
 ; NUMBER OF SEQ ID NOS: 13
 ; SEQ ID NO 2
 ; LENGTH: 437
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION:
 US-10-294-778-2

Query Match 100.0%; Score 50; DB 14; Length 437;
 Best Local Similarity 100.0%; Pred. No. 6.7; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;

Qy 1 ILAKFLHWL 9
 |||||
 Db 30 ILAKFLHWL 38

RESULT 13
 US-10-294-778-10
 ; Sequence 10, Application US/10294778
 ; Publication No. US20030060417A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA

; TITLE OF INVENTION: No. US20030060417A1el Gene Having Reverse Transcriptase Motif
 ; FILE REFERENCE: 46124-5034-US
 ; CURRENT APPLICATION NUMBER: US/10/294,778
 ; CURRENT FILING DATE: 2002-11-15
 ; PRIOR APPLICATION NUMBER: US/09/582,924
 ; PRIOR FILING DATE: 2000-07-07
 ; PRIOR APPLICATION NUMBER: JP 10/13232
 ; PRIOR FILING DATE: 1998-01-08
 ; PRIOR APPLICATION NUMBER: JP 10/33584
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: JP 10/139177
 ; PRIOR FILING DATE: 1998-05-06
 ; PRIOR APPLICATION NUMBER: PCT/JP99/00039
 ; PRIOR FILING DATE: 1999-01-08
 ; NUMBER OF SEQ ID NOS: 13
 ; SEQ ID NO 10
 ; LENGTH: 438
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION:
 US-10-294-778-10

Query Match 100.0%; Score 50; DB 14; Length 438;
 Best Local Similarity 100.0%; Pred. No. 6.8; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;

Qy 1 ILAKFLHWL 9
 |||||
 Db 30 ILAKFLHWL 38

RESULT 14
 US-10-282-960-81
 ; Sequence 81, Application US/10282960
 ; Publication No. US20030143228A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Si-Yi
 ; APPLICANT: Zhaoyang, You
 ; APPLICANT: Schroers, Roland
 ; TITLE OF INVENTION: Human Telomerase Reverse Transcriptase as a Class-II Restricted N
 ; FILE REFERENCE: P02193US1
 ; CURRENT APPLICATION NUMBER: US/10/282,960
 ; CURRENT FILING DATE: 2002-10-29
 ; PRIOR APPLICATION NUMBER: US 60/345,012
 ; PRIOR FILING DATE: 2001-10-29
 ; NUMBER OF SEQ ID NOS: 100
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 81
 ; LENGTH: 500
 ; TYPE: PRT
 ; ORGANISM: Human
 ; FEATURE:
 ; OTHER INFORMATION:
 US-10-282-960-81

Query Match 100.0%; Score 50; DB 14; Length 500;
 Best Local Similarity 100.0%; Pred. No. 7.6; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;

Qy 1 ILAKFLHWL 9
 |||||
 Db 8 ILAKFLHWL 16

RESULT 15
 US-10-044-692-319
 ; Sequence 319, Application US/10044692
 ; Publication No. US20030096344A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cech, Thomas R.
 ; Lingner, Joachim
 ; Nakamura, Toru
 ; Chapman, Karen B.

;; Morin, Gregg B.
;; Harley, Calvin
;; Andrews, William H.
;; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
;; THERAPEUTIC METHODS
;;
;; NUMBER OF SEQUENCES: 335
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend and Crew LLP
;; STREET: Two Embarcadero Center, 8th Floor
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: United States of America
;; ZIP: 94111
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/044,692
;; FILING DATE: 11-Jan-2002
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/912,951
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: US 08/854,050
;; FILING DATE: 09-MAY-1997
;; APPLICATION NUMBER: US 08/851,843
;; FILING DATE: 06-MAY-1997
;; APPLICATION NUMBER: US 08/846,017
;; FILING DATE: 25-APR-1997
;; APPLICATION NUMBER: US 08/844,419
;; FILING DATE: 18-APR-1997
;; APPLICATION NUMBER: US 08/724,643
;; FILING DATE: 01-OCT-1996
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph T.
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-0026000US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;;
;; INFORMATION FOR SEQ ID NO: 319:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 514 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 319:
US-10-044-692-319

Query Match 100.0%; Score 50; DB 14; Length 514;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILAKFLHWL 9
| | | | |
Db 495 ILAKFLHWL 503

Search completed: May 4, 2005, 12:45:56
Job time : 91.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 12:16:58 ; Search time 24 Seconds
(without alignments)
36.081 Million cell updates/sec

Title: US-09-788-110A-1

Perfect score: 50

Sequence: 1 ILAKFLHWL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	1132	2 T03844	telomerase catalyt
2	41	82.0	663	2 T30621	hypothetical prote
3	39	78.0	276	2 B82243	hypothetical prote
4	39	78.0	603	2 D87438	metallopeptidase M
5	39	78.0	989	2 T15397	hypothetical prote
6	38	76.0	863	2 S38140	probable finger pr
7	37	74.0	108	2 AG2505	hypothetical prote
8	37	74.0	120	2 S65536	Ig light chain v r
9	37	74.0	320	2 A82449	conserved hypothet
10	37	74.0	454	2 A90469	probable 4-alpha-L
11	36	72.0	198	2 H90422	transcriptional re
12	36	72.0	249	2 D83047	conserved hypothet
13	36	72.0	345	2 B90600	hypothetical prote
14	36	72.0	378	2 D83945	hypothetical prote
15	36	72.0	484	2 AG1327	L-aspartate oxidas
16	36	72.0	484	2 A11698	L-aspartate oxidas
17	36	72.0	727	2 T10616	hypothetical prote
18	36	72.0	772	2 H85054	hypothetical prote
19	36	72.0	997	2 T39521	hypothetical signa
20	36	72.0	1072	2 S76888	hypothetical prote
21	36	72.0	2535	2 T04824	hypothetical prote
22	36	72.0	2777	2 D96745	hypothetical prote
23	35	70.0	133	2 S57493	cytochrome-c oxida
24	35	70.0	169	2 H70377	hypothetical prote
25	35	70.0	244	2 AB3609	multidrug resistan
26	35	70.0	410	2 H86290	hypothetical prote
27	35	70.0	512	1 ODFP1	cytochrome-c oxida
28	35	70.0	512	1 ODFP1	cytochrome-c oxida
29	35	70.0	513	2 T11999	cytochrome-c oxida

30	35	70.0	516	2 S36008	cytochrome-c oxida
31	35	70.0	516	2 S45351	cytochrome-c oxida
32	35	70.0	517	2 T11302	cytochrome-c oxida
33	35	70.0	518	2 T11536	cytochrome-c oxida
34	35	70.0	518	2 T11766	cytochrome-c oxida
35	35	70.0	908	2 S51293	probable membrane
36	35	70.0	967	2 C70831	probable mmp14 pro
37	35	70.0	1039	2 S76747	hypothetical prote
38	35	70.0	2104	2 D91286	hypothetical prote
39	35	70.0	2104	2 H86127	hypothetical prote
40	34	68.0	102	2 B97775	hypothetical prote
41	34	68.0	122	2 T52448	flowering locus T
42	34	68.0	172	2 T27310	hypothetical prote
43	34	68.0	175	2 T52447	FT protein [valida
44	34	68.0	234	2 AF2748	hypothetical prote
45	34	68.0	270	2 E97529	amino acid ABC tra

ALIGNMENTS

RESULT 1

T03844

telomerase catalytic chain - human

N:Alternate names: telomerase reverse transcriptase

C:Species: Homo sapiens (man)

C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C:Accession: T03844

R:Nakamura, T.M.; Morin, G.B.; Chapman, K.B.; Weinrich, S.L.; Andrews, W.H.; Lingner, J.;

Science 277, 955-959, 1997

A:Title: Telomerase catalytic subunit homologs from fission yeast and human.

A:Reference number: Z15111; MUID:97400623; PMID:9252327

A:Accession: T03844

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-1132 <NAK>

A:Cross-references: UNIPROT:O14746; EMBL:AF015950; NID:g2330016; PIDN:AAC51672.1; PID:g23

A:Experimental source: kidney

C:Genetics:

A:Gene: TRT

A:Map position: 5p

Query Match 100.0%; Score 50; DB 2; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0.54; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 ILAKFLHWL 9

Db 540 ILAKFLHWL 548

RESULT 2

T30621

hypothetical protein 19L - Mollusum contagiosum virus 1

N:Alternate names: MC019L

C:Species: Mollusum contagiosum virus 1

C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 03-Nov-2003

C:Accession: T30621

R:Senkevich, T.G.; Bugert, J.J.; Sieler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.

Science 273, 813-816, 1996

A:Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host res

A:Reference number: Z20876; MUID:96325459; PMID:8670425

A:Accession: T30621

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-663 <SEN>

A:Cross-references: EMBL:U60315; PIDN:AAC55147.1

C:Genetics:

A>Note: MC019L

C:Superfamily: uncharacterized conserved protein

Query Match 82.0%; Score 41; DB 2; Length 663;

Best Local Similarity 66.7%; Pred. No. 13;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ILAKFLHWL 9
: : : : :
Db 260 VIADFLHLW 268

RESULT 3
B82243
hypothetical protein VC1074 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: B82243
R;Heidelber, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
charlson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, B.
L. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: B82243
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-276 <HEI>
A:Cross-references: UNIPROT:Q9KT31; GB:AE004189; GB:AE003852; NID:G9655541; PIDN:AAF9423
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC1074
A:Map position: 1

Query Match 78.0%; Score 39; DB 2; Length 276;
Best Local Similarity 87.5%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LAKFLHLW 9
: : : : :
Db 83 LALFLHLW 90

RESULT 4
D87438
metallopeptidase M24 family protein [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: D87438
R;Niernan, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: D87438
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-603 <STO>
A:Cross-references: UNIPROT:Q9A839; GB:AE005673; NID:G13422906; PIDN:AAK23504.1; GSPDB:G
C:Genetics:
A:Gene: CC1525
C:Superfamily: pig X-Pro aminopeptidase

Query Match 78.0%; Score 39; DB 2; Length 603;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LAKFLHLW 9
: : : : :
Db 331 LTRFLHLW 338

RESULT 5
T15397
hypothetical protein C03F11.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T15397
R;Bentley, D.
submitted to the EMBL Data Library, October 1995
A:Description: The sequence of C. elegans cosmid C03F11.
A:Reference number: Z18342
A:Accession: T15397
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-989 <BEN>
A:Cross-references: EMBL:U39744; NID:G1049465; PID:G1049469; PIDN:AAA80442.1; CESP:C03F11
C:Genetics:
A:Gene: CESP:C03F11.4
A:Introns: 26/1; 57/2; 118/2; 195/2; 284/1; 308/1; 390/1; 407/1; 433/1; 451/3; 547/3; 605/3
A:Introns: 26/1; 57/2; 118/2; 195/2; 284/1; 308/1; 390/1; 407/1; 433/1; 451/3; 547/3; 605/3

Query Match 78.0%; Score 39; DB 2; Length 989;
Best Local Similarity 75.0%; Pred. No. 43;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ILAKFLHW 8
: : : : :
Db 602 IIKKFLHW 609

RESULT 6
S38140
probable finger protein YKR064w - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 16-Aug-2004
C:Accession: S38140
R;van Vliet-Reedijk, J.C.; Planta, R.J.
submitted to the Protein Sequence Database, March 1994
A:Reference number: S38130
A:Accession: S38140
A:Molecule type: DNA
A:Residues: 1-863 <VAN>
A:Cross-references: UNIPROT:P36023; EMBL:Z28289; NID:G486530; PIDN:CAA82143.1; PID:G48653
A:Experimental source: strain S288C
C:Genetics:
A:Cross-references: SGD:S0001772
A:Map position: 11R
C:Superfamily: GAL4 zinc binuclear cluster homology
C:Keywords: DNA binding; nucleus; transcription regulation; zinc finger
F:14-52/Domain: GAL4 zinc binuclear cluster homology <GAL4>
F:19-47/Region: zinc finger

Query Match 76.0%; Score 38; DB 2; Length 863;
Best Local Similarity 75.0%; Pred. No. 57;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ILAKFLHW 8
: : : : :
Db 372 ILLRFLHW 379

RESULT 7
AG2505
hypothetical protein all7223 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120a1
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AG2505
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AG2505
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-108 <KUR>
A:Cross-references: UNIPROT:Q8YKR8; GB:BA000020; PIDN:BAB78307.1; PID:G17135761; GSPDB:G
A:Experimental source: strain PCC 7120
C:Genetics:

A:Gene: all7223
A:Genome: plasmid

Query Match 74.0%; Score 37; DB 2; Length 108;
Best Local Similarity 55.6%; Pred. No. 12;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ILAKFLHWL 9
DB 87 LINKFLHW 95

RESULT 8

ig light chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C:Accession: S66536
R:Tsiotis, G.; Haase, W.; Engel, A.; Michel, H.
Eur. J. Biochem. 231, 823-830, 1995
A:Title: Isolation and structural characterization of trimeric cyanobacterial photosystem II
A:Reference number: S66536; MUID:95377318; PMID:7649183
A:Accession: S66536
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-120 <TSI>
A:CROSS-references: EMBL:X8903; NID:9895870; PIDN:CAA61365.1; PID:g1103702
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 37; DB 2; Length 120;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ILAKFLHW 8
DB 29 ISSKFLHW 36

RESULT 9

conserved hypothetical protein VCA0524 [imported] - Vibrio cholerae (strain N16961 serog O1)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: AB2449
R:Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
l. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: AB2035; MUID:20406833; PMID:10952301
A:Accession: AB2449
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-320 <HE1>
A:CROSS-references: UNIPROT:Q9KM64; GB:AE004383; GB:AE003853; NID:g9657927; PIDN:AAF9642
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VCA0524
A:Map position: 2

Query Match 74.0%; Score 37; DB 2; Length 320;
Best Local Similarity 62.5%; Pred. No. 34;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ILAKFLHW 8
DB 56 VLLKYLHW 63

RESULT 10

AH0469
probable 4-alpha-L-fucosyltransferase [imported] - Yersinia pestis (strain CO92)

C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AH0469
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, I.
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AH0469
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-454 <KUR>
A:CROSS-references: UNIPROT:Q8ZAF1; GB:AL590842; PIDN:CAC93324.1; PID:g15981771; GSPDB:G
C:Genetics:
A:Gene: wecF

Query Match 74.0%; Score 37; DB 2; Length 454;
Best Local Similarity 66.7%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ILAKFLHWL 9
DB 420 VLAKLLYWL 428

RESULT 11

H90422
transcriptional regulator, probable [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: H90422
R:Sheng, Q.; Singh, R.K.; Confalonieri, P.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.;
arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: H90422
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-198 <KUR>
A:CROSS-references: UNIPROT:Q97VV1; GB:AE006641; NID:g13815808; PIDN:AAK42639.1; GSPDB:G
C:Genetics:
A:Gene: SSO2506

Query Match 72.0%; Score 36; DB 2; Length 198;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LAKFLHWL 9
DB 96 LAKFLEWM 103

RESULT 12

DB3047
conserved hypothetical protein PA4790 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 16-Aug-2004
C:Accession: D83047
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bri-
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Llm,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen.
A:Reference number: AB2950; MUID:20437337; PMID:10984043
A:Accession: D83047
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-249 <STO>
A:CROSS-references: UNIPROT:Q9HV18; GB:AE004892; GB:AE004091; NID:g9951049; PIDN:AA08176
A:Experimental source: strain PA01

C;Genetics:
 A;Gene: PA4790
 C;Superfamily: 3-demethylubiquinone-9-3-O-methyltransferase

Query Match 72.0%; Score 36; DB 2; Length 249;
 Best Local Similarity 62.5%; Pred. No. 41;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LAKFLHWL 9
 | : |||||
 Db 238 LGRYHLWL 245

RESULT 13
 B90600
 hypothetical protein MYPV 7060 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
 C;Species: Mycoplasma pulmonis
 C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
 C;Accession: B90600
 R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
 Nucleic Acids Res. 29, 2145-2153, 2001
 A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
 A;Reference number: A99512; MUID:21267165; PMID:11353084
 A;Accession: B90600
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-345 <KUR>
 A;Cross-references: UNIPROT:Q98PL6; GB:AL445566; PID:g14090121; PIDN:CAC13879.1; GSPDB:C
 A;Experimental source: strain UAB CTIP
 C;Genetics:
 A;Gene: MYPV 7060
 A;Genetic code: SGC3

Query Match 72.0%; Score 36; DB 2; Length 345;
 Best Local Similarity 85.7%; Pred. No. 55;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LAKFLHW 8
 | : |||||
 Db 185 LFKFLHW 191

RESULT 14
 D83945
 hypothetical protein BH2364 [imported] - Bacillus halodurans (strain C-125)
 C;Species: Bacillus halodurans
 C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C;Accession: D83945
 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
 Nucleic Acids Res. 28, 4317-4331, 2000
 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A;Reference number: A83650; MUID:20512582; PMID:11058132
 A;Accession: D83945
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-378 <STO>
 A;Cross-references: UNIPROT:Q9KAC5; GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BA8060
 A;Experimental source: strain C-125
 C;Genetics:
 A;Gene: BH2364

Query Match 72.0%; Score 36; DB 2; Length 378;
 Best Local Similarity 75.0%; Pred. No. 60;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LAKFLHWL 9
 | : |||||
 Db 36 LVDFLHWL 43

RESULT 15
 AG1327
 L-aspartate oxidase homolog nadB [imported] - Listeria monocytogenes (strain EGD-e)

C;Species: Listeria monocytogenes
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 16-Aug-2004
 C;Accession: AG1327
 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
 D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;
 Science 294, 849-852, 2001
 A;Authors: Krefte, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
 ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
 A;Title: Comparative genomics of Listeria species.
 A;Reference number: AB1077; MUID:21537279; PMID:11679669
 A;Accession: AG1327
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-484 <GLA>
 A;Cross-references: UNIPROT:O8Y5N4; GB:NC_003210; PIDN:CAD00101.1; PID:g16411493; GSPDB:B
 A;Experimental source: strain EGD-e
 C;Genetics:
 A;Gene: nadB
 C;Superfamily: Succinate dehydrogenase flavoprotein subunit; 3-oxosteroid 1-dehydrogenase

Query Match 72.0%; Score 36; DB 2; Length 484;
 Best Local Similarity 62.5%; Pred. No. 76;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LAKFLHWL 9
 | : |||||
 Db 430 ITEFLHWL 437

Search completed: May 4, 2005, 12:28:59
 Job time : 26 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 12:08:43 ; Search time 112.5 Seconds
(without alignments)
40.966 Million cell updates/sec

Title: US-09-788-110A-1
Perfect score: 50
Sequence: 1 ILAKFLHWL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	50	100.0	795	2	Q8NG38	Q8ng38 homo sapien
2	50	100.0	807	2	Q8N6C3	Q8n6c3 homo sapien
3	50	100.0	1069	2	Q8NG46	Q8ng46 homo sapien
4	50	100.0	1132	1	TERT HUMAN	O14746 homo sapien
5	45	90.0	141	2	Q8RG60	Q8rg60 fusobacteri
6	44	88.0	1346	2	Q8RD80	Q8rd80 gallus gall
7	41	82.0	77	2	Q8EIB9	Q8eib9 stewanella
8	41	82.0	301	2	O11310	O11310 molluscum c
9	41	82.0	663	2	Q98188	Q98188 molluscum c
10	39	78.0	197	2	Q9G782	Q9g782 xylocopa va
11	39	78.0	276	2	Q9KT31	Q9kt31 vibrio chol
12	39	78.0	324	2	Q9XKG9	Q9xkg9 oecophylla
13	39	78.0	410	2	Q8EF88	Q8ef88 hyposproxa
14	39	78.0	603	2	Q9A839	Q9a839 caulobacter
15	39	78.0	702	2	Q8CUD6	Q8cud6 kluyveromyc
16	38	76.0	165	2	Q6PWJ3	Q6pwj3 raja ocella
17	38	76.0	176	2	Q8MGU0	Q8mgu0 litoria fal
18	38	76.0	347	2	Q8DI95	Q8di95 synecococc
19	38	76.0	448	2	Q6DVM4	Q6dvm4 triops long
20	38	76.0	521	2	Q7N5R0	Q7n5r0 photorhabdu
21	38	76.0	863	1	YK44 YEAST	P36023 saccharomyc
22	38	76.0	1191	2	Q9DE32	Q9de32 xenopus lae
23	37	74.0	43	2	Q8CON6	Q8cm6 staphylococ
24	37	74.0	77	2	Q8RUN8	Q8run8 oryza sativ
25	37	74.0	104	2	Q7YI16	Q7yil6 pemphigus o
26	37	74.0	108	2	Q7YI17	Q7yil7 pemphigus o
27	37	74.0	108	2	Q8YKR8	Q8ykr8 anabaena sp
28	37	74.0	109	2	Q7YI15	Q7yil5 pemphigus o
29	37	74.0	111	2	Q7Y7N7	Q7y7n7 pemphigus o
30	37	74.0	111	2	Q85PD3	Q8spd3 pemphigus p
31	37	74.0	123	2	Q8HH27	Q8hh27 crematogast

32	37	74.0	140	2	Q6XLJ1	Q6xlj1 lasius turc
33	37	74.0	143	2	Q8HH37	Q8hh37 crematogast
34	37	74.0	147	2	Q8HH31	Q8hh31 crematogast
35	37	74.0	153	2	Q8HH13	Q8hh13 crematogast
36	37	74.0	153	2	Q8HH14	Q8hh14 crematogast
37	37	74.0	154	2	Q8HH15	Q8hh15 crematogast
38	37	74.0	154	2	Q8HH16	Q8hh16 crematogast
39	37	74.0	154	2	Q8HH19	Q8hh19 crematogast
40	37	74.0	154	2	Q8HH26	Q8hh26 crematogast
41	37	74.0	154	2	Q8HH30	Q8hh30 crematogast
42	37	74.0	154	2	Q8HH33	Q8hh33 crematogast
43	37	74.0	154	2	Q8HH39	Q8hh39 crematogast
44	37	74.0	157	2	Q8HAX2	Q8hax2 crematogast
45	37	74.0	157	2	Q8HH29	Q8hh29 crematogast

ALIGNMENTS

RESULT 1
Q8NG38 PRELIMINARY; PRT; 795 AA.
AC Q8NG38;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE ABG-deleted variant of telomerase reverse transcriptase.
GN Name=TERT;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RA Hisatomi H., Ohvashiki K., Ohvashiki J.H., Nagao K., Kanamaru T.,
RA Hirata H., Hibi N., Tsukada Y.;
RT "Expression profile of a gamma-deletion variant of the human
RT telomerase reverse transcriptase gene.";
RL Neoplasia 5:193-197(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RA Nagao K., Katsumata K., Aizawa Y., Saito N., Hirata H., Sasaki H.,
RA Yamamoto S., Hikiiji K., Koira T., Hisatomi H.;
RT "Differential alternative splicing expressions of telomerase reverse
RT transcriptase in gastrointestinal cell lines.";
RL Oncol. Rep. 11:127-131(2004).
DR EMBL; AB086950; BAC11015.1;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. . .; IEA.
DR InterPro; IP0003545; Telomerase_RT.
DR PRINTS; PR01365; TelomeraseRT.
KW RNA-directed DNA polymerase.
SQ SEQUENCE 795 AA; 88964 MW; 6BEAC8A6D1A2E8CB CRC64;

Query Match 100.0%; Score 50; DB 2; Length 795;
Best Local Similarity 100.0%; Pred. No. 1.7; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;
Qy 1 ILAKFLHWL 9
Db 540 ILAKFLHWL 548

RESULT 2
Q8N6C3 PRELIMINARY; PRT; 807 AA.
ID Q8N6C3
AC Q8N6C3;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)


```
RT telomerase RNA and TEP1 binding."
RL Mol. Biol. Cell 11:3329-3340(2000).
CC -!- FUNCTION: Telomerase is a ribonucleoprotein enzyme essential for
CC the replication of chromosome termini in most eukaryotes. It
CC elongates telomeres. It is a reverse transcriptase that adds
CC simple sequence repeats to chromosome ends by copying a template
CC sequence within the RNA component of the enzyme.
CC -!- SUBUNIT: Component of the telomerase ribonucleoprotein complex at
CC least composed of TEP1, EST1A, POT1 and a telomerase RNA template
CC component (TER). Interacts with PINX1.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DISEASE: Activation of telomerase has been implicated in cell
CC immortalization and cancer cell pathogenesis.
CC -!- SIMILARITY: Belongs to the reverse transcriptase family.
CC Telomerase subfamily.
CC -!- SIMILARITY: Contains 1 reverse transcriptase domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch)
CC -----
DR EMBL; AF015950; AAC51672.1; -.
DR EMBL; AF018167; AAC51724.1; -.
DR EMBL; AF128894; AAD30037.1; -.
DR EMBL; AF128893; AAD30037.1; JOINED.
DR EMBL; AY007685; AAG23289.1; -.
DR PIR; T03844; T03844.
DR Genew; HGNC:11730; TERT.
DR MIM; 187270; -.
DR GO; GO:0000781; C:chromosome, telomeric region; TAS.
DR GO; GO:0042162; F:telomeric DNA binding; TAS.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. . .; TAS.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; RVT; 1.
DR PRINTS; PR01365; TELOMERASERT.
DR PROSITE; PS0878; RT_P0L; 1.
KW DNA-binding; Nuclear protein; Ribonucleoprotein;
KW RNA-directed DNA polymerase; Telomere; Transcriptase.
FT DOMAIN 605 935
FT MUTAGEN 868 869 D->A: Loss of telomerase activity.
FT MUTAGEN 868 869 DD->AA: Loss of telomerase activity.
FT MUTAGEN 869 869 D->A: Loss of telomerase activity.
FT MUTAGEN 712 712 D->A: Loss of telomerase activity.
FT CONFLICT 516 516 D -> G (in Ref. 2).
SQ SEQUENCE 1132 AA; 126996 MW; 94E35469C4CA33A0 CRC64;

Query Match 100.0%; Score 50; DB 1; Length 1132;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILAKFLHWL 9
| | | | |
Db 540 ILAKFLHWL 548

RESULT 5
Q8RG60 PRELIMINARY; PRT; 141 AA.
AC Q8RG60;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein FN0457.
OS OrderedLocustNames=FN0457;
OC Fusobacterium nucleatum (subsp. nucleatum).
OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
OX NCBI_TaxID=76856;
```

```
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=ATCC 25586;
RX MEDLINE=21886394; PubMed=1189109;
RX DOI=10.1128/JB.184.7.2005-2018.2002;
RA Kapatral V., Anderson I., Ivanova N., Reznik G., Lykidis A.,
RA Bhattacharya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
RA Vasieva O., Chu L., Kogan Y., Chaga O., Goltzman E., Bernal A.,
RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
RA Fonstein M., Kyrpides N.C., Overbeek R.;
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
RL J. Bacteriol. 184:2005-2018(2002).
DR EMBL; AB010557; AAL94653.1; -.
KW Complete proteome.
SQ SEQUENCE 141 AA; 16999 MW; FE4ADE5A6C0666FF CRC64;

Query Match 90.0%; Score 45; DB 2; Length 141;
Best Local Similarity 77.8%; Pred. No. 2.8;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILAKFLHWL 9
| | | | |
Db 133 ILAKFLHWL 141

RESULT 6
Q8RD80 PRELIMINARY; PRT; 1346 AA.
AC Q8RD80;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Telomerase reverse transcriptase.
GN Name=TERT;
OS Gallus gallus gallus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=208526;
[1]
RN SEQUENCE FROM N.A.
RC PubMed=15363846;
RA Delany M.E., Daniels L.M.;
RT "The chicken telomerase reverse transcriptase (chTERT): molecular and
RT cytogenetic characterization with a comparative analysis.";
RL Gene 339:61-69(2004).
DR EMBL; AY502592; AAS75793.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. . .; IEA.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; RVT; 1.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase; Transcriptase.
SQ SEQUENCE 1346 AA; 155316 MW; E93A8B64F66A4D40 CRC64;

Query Match 88.0%; Score 44; DB 2; Length 1346;
Best Local Similarity 88.9%; Pred. No. 35;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILAKFLHWL 9
| | | | |
Db 749 ILAKFLHWL 757

RESULT 7
Q8EIB9 PRELIMINARY; PRT; 77 AA.
ID Q8EIB9
AC Q8EIB9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
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DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein SO0924.
CN OrderedLocustNames=SO0924;
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Shewanellaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MR-1;
RX MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;
RA Heidelberg J.P., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,
RA Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M.J.,
RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,
RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M.,
RA Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,
RA Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
RA Venter J.C., Neilson K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis.";
RL Nat. Biotechnol. 20:1118-1123(2002).
DR EMBL; AE015537; AAN5398.1; -.
DR TIGR; SO0924; -.
KW Complete proteome.
SQ SEQUENCE 77 AA; 8773 MW; D05BDC05EE6988CC CRC64;

Query Match 82.0%; Score 41; DB 2; Length 77;
Best Local Similarity 87.5%; Pred. No. 8.5;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LAKFLHWL 9
Db 11 LKFLHWL 18

RESULT 8
ID O11310 PRELIMINARY; PRT; 301 AA.
AC O11310;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE B1-12 protein (Fragment).
GN Name=B1-12;
OS Molluscum contagiosum virus subtype 1 (NCVI).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Molluscipoxvirus.
OX NCBI_TaxID=10280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97352177; PubMed=9208457; DOI=10.1023/A:1007991508159;
RA Moratilla M., Agromayor M., Nunez A., Funes J.M., Varas A.J.,
RA Lopez-Esteban J.L., Esteban M., Martin-Gallardo A.;
RT "A random DNA sequencing, computer-based approach for the generation
RT of a gene map of molluscum contagiosum virus.";
RL Virus Genes 14:73-80(1997).
DR EMBL; U86895; AAB57940.1; -.
DR GO; GO:0016032; P:Viral life cycle; IEA.
DR InterPro; IPR005005; Pox_F12L.
DR Pfam; PF03337; Pox_F12L_1.
FT NON TER 301
SQ SEQUENCE 301 AA; 33606 MW; C21BBE05E31189A CRC64;

Query Match 82.0%; Score 41; DB 2; Length 301;
Best Local Similarity 66.7%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ILAKFLHWL 9
Db 260 VIADFLHWL 268

RESULT 9
ID Q98188 PRELIMINARY; PRT; 663 AA.
AC Q98188;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE MC019L.
GN Name=MC019L;
OS Molluscum contagiosum virus subtype 1 (NCVI).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Molluscipoxvirus.
OX NCBI_TaxID=10280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96325459; PubMed=8670425;
RA Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G.,
RA Moss B.;
RT "Genome sequence of a human tumorigenic poxvirus: prediction of
RT specific host response-evasion genes.";
RL Science 273:813-816(1996).
DR EMBL; U60315; AAC55147.1; -.
DR PIR; T30621; T30621.
DR GO; GO:0016032; P:Viral life cycle; IEA.
DR InterPro; IPR005005; Pox_F12L.
DR Pfam; PF03337; Pox_F12L_1.
DR PIRSF; PIRSF015793; VAC_EEV; 1.
SQ SEQUENCE 663 AA; 73099 MW; 7EAll9E8A5FFFFF19 CRC64;

Query Match 82.0%; Score 41; DB 2; Length 663;
Best Local Similarity 66.7%; Pred. No. 63;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ILAKFLHWL 9
Db 260 VIADFLHWL 268

RESULT 10
ID Q9G782 PRELIMINARY; PRT; 197 AA.
AC Q9G782;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Cytochrome oxidase subunit 1 (Fragment).
GN Name=COI;
OS Xylocopa varipuncta.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Xylocopa.
OX NCBI_TaxID=135685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20575774; PubMed=11133195; DOI=10.1006/mpev.2000.0851;
RA Leys R., Cooper S.J.B., Schwarz M.P.;
RT "Molecular phylogeny of the large carpenter bees, genus Xylocopa
RT (Hymenoptera: apidae), based on mitochondrial DNA sequences.";
RL Mol. Phylogenet. Evol. 17:407-418(2000).
CC -1- FUNCTION: Cytochrome c oxidase is the component of the respiratory
CC chain that catalyzes the reduction of oxygen to water. Subunits 1-
CC 3 form the functional core of the enzyme complex. CO I is the
CC catalytic subunit of the enzyme. Electrons originating in
CC cytochrome c are transferred via the copper A center of subunit 2
CC and heme A of subunit 1 to the bimetallic center formed by heme A3
CC and copper B (By similarity).
CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -1- PATHWAY: Respiratory chain; terminal step.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial

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CC inner membrane (By similarity).
CC -!- SIMILARITY: Belongs to the heme-copper respiratory oxidase family.
DR EMBL; AY005245; AAG24251.1; -.
DR GO; GO:0019866; C:inner membrane; IEA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
DR GO; GO:0005739; C:cytochrome c oxidase; IEA.
DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; F:electron transport; IEA.
DR GO; GO:0006810; F:transport; IEA.
DR InterPro; IPR000883; COX1.
DR Pfam; PF00115; COX1; 1.
DR PRINTS; PR01165; CYCOXIDASEI.
DR Copper; Electron transport; Heme; Inner membrane; Membrane;
KW Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
KW Transport.
FT NON_TER 1 1
FT NON_TER 197 197
SQ SEQUENCE 197 AA; 22799 MW; 524729587C51DEB7 CRC64;

Query Match 78.0%; Score 39; DB 2; Length 197;
Best Local Similarity 62.5%; Pred. No. 47;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILAKPLHW 8
DB 78 IISKFIHW 85

RESULT 11
OQKT31 PRELIMINARY; PRT; 276 AA.
AC OQKT31;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Hypothetical protein VC1074.
GN OrderedlocusNames=VC1074;
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Unayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L.,
RA Ermolaeva M.D., Vamathevan J.J., Bass S., Qin H., Dragoi I.,
RA Sellers P., McDonald L.A., Utterback T.R., Fleischmann R.D.,
RA Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R.,
RA Mekalanos J.J., Venter J.C., Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae."
RL Nature 406:477-483(2000).
RL EMBL; AE004189; AAF94233.1; -.
DR PIR; B82243; B82243.
DR TIGR; VC1074; -.
DR InterPro; IPR003675; Abi.
DR Pfam; PF02517; Abi; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 276 AA; 30242 MW; B518085AF2EB7CAF CRC64;

Query Match 78.0%; Score 39; DB 2; Length 276;
Best Local Similarity 87.5%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LAKFLHWL 9
DB 83 LALFLHWL 90

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RESULT 12
Q9XKG9 PRELIMINARY; PRT; 324 AA.
AC Q9XKG9;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Cytochrome oxidase subunit 1 (Fragment).
OS Oecophylla smaragdina.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Formicidae; Formicinae; Oecophylla.
OX NCBI_TaxID=84561;
RN [1]
RP SEQUENCE FROM N.A.
RA Sameshima S., Hasegawa E., Kitade O., Minaka N., Matsumoto T.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory
CC chain that catalyzes the reduction of oxygen to water. Subunits 1-
CC 3 form the functional core of the enzyme complex. CO 1 is the
CC catalytic subunit of the enzyme. Electrons originating in
CC cytochrome c are transferred via the copper A center of subunit 2
CC and heme A of subunit 1 to the bimetallic center formed by heme A3
CC and copper B (By similarity).
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferrocycytochrome
CC c + 2 H(2)O.
CC -!- PATHWAY: Respiratory chain; terminal step.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane (By similarity).
CC -!- SIMILARITY: Belongs to the heme-copper respiratory oxidase family.
DR EMBL; AB019426; BAA76733.1; -.
DR GO; GO:0019866; C:inner membrane; IEA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
DR GO; GO:0005739; C:cytochrome c oxidase; IEA.
DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; F:electron transport; IEA.
DR InterPro; IPR000883; COX1.
DR Pfam; PF00115; COX1; 1.
DR PRINTS; PR01165; CYCOXIDASEI.
DR PROSITE; PS00077; COX1_CUB; 1.
KW Copper; Electron transport; Heme; Inner membrane; Membrane;
KW Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
FT NON_TER 1 1
FT NON_TER 324 324
SQ SEQUENCE 324 AA; 35901 MW; 49CD3A88D000CF2C CRC64;

Query Match 78.0%; Score 39; DB 2; Length 324;
Best Local Similarity 75.0%; Pred. No. 74;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ILAKPLHW 8
DB 307 ILAGPLHW 314

RESULT 13
Q9E8F8 PRELIMINARY; PRT; 410 AA.
AC Q9E8F8;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Cytochrome oxidase subunit 1 (fragment).
GN Name=COI;
OS Hypsoprora sp. CPL-2004.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

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CC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Membracidae;
 CC Membracidae; Hypsopora.
 CC NCBI_TaxID=269930;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lin C.-P., Danforth B.N., Wood T.K.;
 RT "Molecular phylogenetics and evolution of maternal care in membracine
 treehoppers";
 RL Syst. Biol. 53:400-421(2004).
 CC -1- FUNCTION: Cytochrome c oxidase is the component of the respiratory
 CC chain that catalyzes the reduction of oxygen to water. Subunits 1-
 CC 3 form the functional core of the enzyme complex. CO I is the
 CC catalytic subunit of the enzyme. Electrons originating in
 CC cytochrome c are transferred via the copper A center of subunit 2
 CC and heme A of subunit 1 to the bimetallic center formed by heme A3
 CC and copper B (By similarity).
 CC -1- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -1- PATHWAY: Respiratory chain; terminal step.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane (By similarity).
 CC -1- SIMILARITY: Belongs to the heme-copper respiratory oxidase family.
 DR EMBL; AY513407; AAT11352.1; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR000883; COX1.
 DR Pfam; PF00115; COX1.1.
 DR PRINTS; PR01165; CYCOXIDASE1.
 DR PROSITE; PS00077; COX1_CUB; 1.
 KW Copper; Electron transport; Heme; Inner membrane; Membrane;
 KW Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
 KW Transport.
 FT NON_TER
 SQ SEQUENCE 410 AA; 45935 MW; 7DB9944D253FCE2C CRC64;
 Query Match 78.0%; Score 39; DB 2; Length 410;
 Best Local Similarity 75.0%; Pred. No. 93;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 ILAKFLHW 8
 Db 286 ILASFIHW 293
 RESULT 14
 Q9A839 PRELIMINARY; PRT; 603 AA.
 AC Q9A839;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Metalloproteinase M24 family protein.
 GN OrderedLocustNames=CC1525;
 OS Caulobacter crescentus.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
 OC Caulobacteraceae; Caulobacter.
 CC NCBI_TaxID=155892;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 19089 / CB15;
 RX MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
 RA Nieman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 RA Eisen J.A., Heideberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
 RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
 RA Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,
 RA Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
 RA Ermlaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
 RA Fraser C.M.;
 RT "Complete genome sequence of Caulobacter crescentus.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

DR EMBL; AE005827; AAK23504.1; -.
 DR PIR; D87438; D87438.
 DR MEROPS; M24.009; -.
 DR TIGR; CC1525; -.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0008235; F:metalloproteinase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR002086; Aldehyd dehydrog.
 DR InterPro; IPR000994; Peptidase M24.
 DR Pfam; PF00557; Peptidase M24; 1.
 DR PROSITE; PS00687; ALDEHYDE_DEHYD_GLU; UNKNOWN_1.
 KW Complete proteome; Hydrolase.
 SQ SEQUENCE 603 AA; 64341 MW; EC7D18169D9978DC CRC64;
 Query Match 78.0%; Score 39; DB 2; Length 603;
 Best Local Similarity 75.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 LAKFLHWL 9
 Db 331 LTRFLHWL 338
 RESULT 15
 Q6CUD6 PRELIMINARY; PRT; 702 AA.
 ID Q6CUD6;
 AC Q6CUD6;
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Similar to sp|P38315 Saccharomyces cerevisiae YBR216C.
 GN ORFNames=KLLA0C05698g;
 OS Kluyveromyces lactis NRRL Y-1140.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 CC NCBI_TaxID=284590;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-1140;
 RG Genolevures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neugeglise C., Talia E.,
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boisrame A., Boyer J., Cattolico L., Confaniolieri F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicaud J.M., Nikolaki M., Oztas S., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
 RA Swennene D., Tekia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
 RA Wincker P., Souciet J.L.;
 RT "Genome evolution in yeasts.";
 RL Nature 430:35-44(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-1140;
 RA Genoscope;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR382123; CAH01304.1; -.
 SQ SEQUENCE 702 AA; 80513 MW; F7AA23F2078CFE8D CRC64;
 Query Match 78.0%; Score 39; DB 2; Length 702;
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 ILAKFLHW 8
 Db 77 ILIKFIHW 84

Thu May 12 09:52:38 2005

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Search completed: May 4, 2005, 12:28:06
Job time : 114.5 secs

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OM protein - protein search, using sw model

Run on: May 4, 2005, 12:20:14 ; Search time 30 Seconds
(without alignments)
22.395 Million cell updates/sec

Title: US-09-788-110A-2

Perfect score: 43

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Scoring table: BLOSUM62

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	100.0	13	3	US-08-974-549A-77
2	43	100.0	13	4	US-08-912-951-77
3	43	100.0	13	4	US-09-402-181B-77
4	43	100.0	13	4	US-09-721-456-77
5	43	100.0	17	4	US-09-042-460-25
6	43	100.0	22	3	US-08-851-843A-170
7	43	100.0	22	3	US-08-974-549A-290
8	43	100.0	22	3	US-08-854-050-170
9	43	100.0	22	3	US-09-430-323-170
10	43	100.0	22	4	US-09-402-181B-290
11	43	100.0	22	4	US-09-721-456-290
12	43	100.0	22	4	US-09-766-253-170
13	43	100.0	43	3	US-08-974-549A-34
14	43	100.0	43	4	US-08-912-951-34
15	43	100.0	43	4	US-09-402-181B-34
16	43	100.0	43	4	US-09-721-456-34
17	43	100.0	267	4	US-09-248-796A-15792
18	43	100.0	364	4	US-09-417-485D-40
19	43	100.0	364	4	US-09-417-485D-49
20	43	100.0	438	4	US-09-582-924B-10
21	43	100.0	538	3	US-08-974-549A-602
22	43	100.0	538	4	US-08-912-951-316
23	43	100.0	538	4	US-09-402-181B-602
24	43	100.0	538	4	US-09-721-456-602
25	43	100.0	564	3	US-08-851-843A-101
26	43	100.0	564	3	US-08-974-549A-267
27	43	100.0	564	3	US-08-854-050-101

28	43	100.0	564	3	US-09-430-323-101	Sequence 101, App
29	43	100.0	564	4	US-09-402-181B-267	Sequence 267, App
30	43	100.0	564	4	US-09-721-456-267	Sequence 267, App
31	43	100.0	564	4	US-09-766-253-101	Sequence 101, App
32	43	100.0	622	4	US-09-582-924B-12	Sequence 12, App
33	43	100.0	867	4	US-09-417-485D-2	Sequence 2, Appl
34	43	100.0	867	4	US-09-417-485D-4	Sequence 4, Appl
35	43	100.0	1003	3	US-08-851-843A-217	Sequence 217, App
36	43	100.0	1003	3	US-08-974-549A-336	Sequence 336, App
37	43	100.0	1003	3	US-08-854-050-217	Sequence 217, App
38	43	100.0	1003	3	US-09-430-323-217	Sequence 217, App
39	43	100.0	1003	4	US-09-402-181B-336	Sequence 336, App
40	43	100.0	1003	4	US-09-721-456-336	Sequence 336, App
41	43	100.0	1132	3	US-08-851-843A-225	Sequence 225, App
42	43	100.0	1132	3	US-08-974-549A-2	Sequence 2, Appl
43	43	100.0	1132	3	US-08-974-549A-344	Sequence 344, App
44	43	100.0	1132	3	US-08-854-050-225	Sequence 225, App
45	43	100.0	1132	3	US-09-430-323-225	Sequence 225, App

ALIGNMENTS

RESULT 1

US-08-974-549A-77
; Sequence 77, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951

;
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..13
; OTHER INFORMATION: /note= "telomerase RT palm, primer grip"
; OTHER INFORMATION: motif C peptide from human TRT"
; US-08-974-549A-77

Query Match 100.0%; Score 43; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLVDFFLLV 9
Db 4 RLVDFFLLV 12

RESULT 2
US-08-912-951-77
; Sequence 77, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,951
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050

;
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..13
; OTHER INFORMATION: /note= "telomerase RT palm, primer grip"
; OTHER INFORMATION: motif C peptide from human TRT"
; US-08-912-951-77

Query Match 100.0%; Score 43; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLVDFFLLV 9
Db 4 RLVDFFLLV 12

RESULT 3
US-09-402-181B-77
; Sequence 77, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

APPLICANT: Depinho, Ronald
APPLICANT: Greenberg, Roger
TITLE OF INVENTION: Mouse Telomerase Reverse Transcriptase
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,460
FILING DATE: 16-MAR-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/979,742
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 015389-0031110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-09-042-460-25
Query Match 100.0%; Score 43; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RLVDDFLLV 9
Db 3 RLVDDFLLV 11
RESULT 6
US-08-851-843A-170
; Sequence 170, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 170:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1-22
; OTHER INFORMATION: /note= "motif C peptide from human
; OTHER INFORMATION: telomerase core protein 1 (TCPL)"
US-08-851-843A-170

Query Match 100.0%; Score 43; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLVDFFLLV 9
Db 8 RLVDFFLLV 16

RESULT 7

US-08-974-549A-290
; Sequence 290, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002610US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 290:

SEQUENCE CHARACTERISTICS:

LENGTH: 22 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..22

OTHER INFORMATION: /note= "motif C peptide from human

OTHER INFORMATION: telomerase core protein 1 (TCPL)"

US-08-974-549A-290

Query Match 100.0%; Score 43; DB 3; Length 22;

Best Local Similarity 100.0%; Pred. No. 0.064;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLVDFFLLV 9

Db 8 RLVDFFLLV 16

RESULT 8

US-08-854-050-170
; Sequence 170, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: NO. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536

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;
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 170:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..22
; OTHER INFORMATION: /note= "motif C peptide from human
; telomerase core protein 1 (TCPI)"
; US-08-854-050-170
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; Query Match 100.0%; Score 43; DB 3; Length 22;
; Best Local Similarity 100.0%; Pred. No. 0.064;
; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 RLVDFFLLV 9
; Db 8 RLVDFFLLV 16
;
; RESULT 9
; US-09-430-323-170
; Sequence 170, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: No. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/430,323
; FILING DATE: 29-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
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; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 170:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..22
; OTHER INFORMATION: /note= "motif C peptide from human
; telomerase core protein 1 (TCPI)"
; US-09-430-323-170
;
; Query Match 100.0%; Score 43; DB 3; Length 22;
; Best Local Similarity 100.0%; Pred. No. 0.064;
; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Qy 1 RLVDFFLLV 9
; Db 8 RLVDFFLLV 16
;
; RESULT 10
; US-09-402-181B-290
; Sequence 290, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181B
; FILING DATE: 29-Sep-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
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;; FILING DATE: 14-AUG-1997
;; APPLICATION NUMBER: US 08/915,503
;; FILING DATE: 14-AUG-1997
;; APPLICATION NUMBER: WO PCT/US97/17885
;; FILING DATE: 01-OCT-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ausehus, Scott L.
;; REGISTRATION NUMBER: 42,271
;; REFERENCE/DOCKET NUMBER: 015389-002620US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 290:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 22 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Peptide
;; LOCATION: 1..22
;; OTHER INFORMATION: /note= "motif C peptide from human
;; telomerase core protein 1 (TCPI)"
;; SEQUENCE DESCRIPTION: SEQ ID NO: 290:
US-09-402-181B-290

Query Match 100.0%; Score 43; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLVDVDFLLV 9
Db 8 RLVDVDFLLV 16

RESULT 11
US-09-721-456-290
; Sequence 290, Application US/09721456
; Patent No. 6617110
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 22-Nov. 6617110-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997

;; APPLICATION NUMBER: US 08/846,017
;; FILING DATE: 25-APR-1997
;; APPLICATION NUMBER: US 08/851,843
;; FILING DATE: 06-MAY-1997
;; APPLICATION NUMBER: US 08/854,050
;; FILING DATE: 09-MAY-1997
;; APPLICATION NUMBER: US 08/911,312
;; FILING DATE: 14-AUG-1997
;; APPLICATION NUMBER: US 08/912,951
;; FILING DATE: 14-AUG-1997
;; APPLICATION NUMBER: US 08/915,503
;; FILING DATE: 14-AUG-1997
;; APPLICATION NUMBER: WO PCT/US97/17618
;; FILING DATE: 01-OCT-1997
;; APPLICATION NUMBER: WO PCT/US97/17885
;; FILING DATE: 01-OCT-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph Ted
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-002610US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 290:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 22 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Peptide
;; LOCATION: 1..22
;; OTHER INFORMATION: /note= "motif C peptide from human
;; telomerase core protein 1 (TCPI)"
;; SEQUENCE DESCRIPTION: SEQ ID NO: 290:
US-09-721-456-290

Query Match 100.0%; Score 43; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLVDVDFLLV 9
Db 8 RLVDVDFLLV 16

RESULT 12
US-09-766-253-170
; Sequence 170, Application US/09766253
; Patent No. 6808880
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. 6808880el Telomerase
; NUMBER OF SEQUENCES: 171
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: 015389-00261005
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

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;
; TOPOLOGY: linear
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; MOLECULE TYPE: peptide
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; FEATURE:
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; NAME/KEY. Peptide

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RESULT 14
US-08-912-951-34
; Sequence 34, Application US/08912951

APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.

; TYPE OF INTERVIEW: AMERICAN BUREAU METHODS
 ; NUMBER OF SEQUENCES: 335
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS:
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..43
OTHER INFORMATION: /note= "motif C and D peptide from human TRT"
US-08-912-951-34

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Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLVDFFLLV 9
Db 3 RLVDFFLLV 11

RESULT 15
US-09-402-181B-34
; Sequence 34, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru

Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Aussenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..43
OTHER INFORMATION: /note= "motif C and D peptide from human TRT"
US-09-402-181B-34

Query Match 100.0%; Score 43; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLVDFFLLV 9
Db 3 RLVDFFLLV 11

Search completed: May 4, 2005, 12:41:38

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 12:28:20 ; Search time 91.5 Seconds
(without alignments)
32.765 Million cell updates/sec

Title: US-09-788-110A-2

Perfect score: 43

Sequence: 1 RLVDFFLLV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

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Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	43	100.0	9	US-09-815-346-9	Sequence 9, Appli
2	43	100.0	9	US-09-872-832-47	Sequence 47, Appli
3	43	100.0	9	US-09-788-110A-2	Sequence 2, Appli
4	43	100.0	9	US-10-080-013-35	Sequence 35, Appli
5	43	100.0	9	US-10-371-942-6	Sequence 6, Appli
6	43	100.0	9	US-10-447-161-95	Sequence 95, Appli
7	43	100.0	9	US-10-289-566-35	Sequence 35, Appli
8	43	100.0	9	US-10-396-578-9	Sequence 9, Appli
9	43	100.0	13	US-10-044-692-77	Sequence 77, Appli
10	43	100.0	13	US-10-044-539-77	Sequence 77, Appli
11	43	100.0	13	US-10-325-810-77	Sequence 77, Appli
12	43	100.0	13	US-10-877-146-77	Sequence 77, Appli
13	43	100.0	17	US-10-282-960-68	Sequence 68, Appli

14	43	100.0	22	9	US-09-843-676-170	Sequence 170, App
15	43	100.0	22	9	US-09-766-253-170	Sequence 170, App
16	43	100.0	22	10	US-09-438-486-170	Sequence 170, App
17	43	100.0	22	14	US-10-053-758-170	Sequence 170, App
18	43	100.0	22	14	US-10-054-295-170	Sequence 170, App
19	43	100.0	22	14	US-10-054-611-170	Sequence 170, App
20	43	100.0	22	15	US-10-325-810-290	Sequence 290, App
21	43	100.0	22	17	US-10-877-146-290	Sequence 290, App
22	43	100.0	22	14	US-10-044-692-34	Sequence 34, Appli
23	43	100.0	43	14	US-10-044-539-34	Sequence 34, Appli
24	43	100.0	43	15	US-10-325-810-34	Sequence 34, Appli
25	43	100.0	43	17	US-10-877-146-34	Sequence 4, Appli
26	43	100.0	174	14	US-10-282-960-4	Sequence 40, Appli
27	43	100.0	364	14	US-10-304-095-40	Sequence 49, Appli
28	43	100.0	364	14	US-10-304-095-49	Sequence 49, Appli
29	43	100.0	438	14	US-10-294-778-10	Sequence 10, Appli
30	43	100.0	500	14	US-10-282-960-81	Sequence 81, Appli
31	43	100.0	538	14	US-10-044-539-316	Sequence 316, App
32	43	100.0	538	14	US-10-044-539-316	Sequence 316, App
33	43	100.0	538	15	US-10-325-810-602	Sequence 602, App
34	43	100.0	538	17	US-10-877-146-602	Sequence 602, App
35	43	100.0	564	9	US-09-843-676-101	Sequence 101, App
36	43	100.0	564	9	US-09-766-253-101	Sequence 101, App
37	43	100.0	564	10	US-09-438-486-101	Sequence 101, App
38	43	100.0	564	14	US-10-053-758-101	Sequence 101, App
39	43	100.0	564	14	US-10-054-295-101	Sequence 101, App
40	43	100.0	564	14	US-10-054-611-101	Sequence 101, App
41	43	100.0	564	15	US-10-325-810-267	Sequence 267, App
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43	43	100.0	867	14	US-10-294-778-12	Sequence 2, Appli
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ALIGNMENTS

RESULT 1

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US-09-815-346-9
; Sequence 9, Application US/09815346
; Publication No. US20020018806A1
; GENERAL INFORMATION:
; APPLICANT: AGRAWAL, BABITA
; APPLICANT: LONGENECKER, MICHAEL B.
; TITLE OF INVENTION: LIPOPEPTIDE ADJUVANTS
; FILE REFERENCE: 042881/0160
; CURRENT APPLICATION NUMBER: US/09/815,346
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/191,736
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Telomerase-derived
; OTHER INFORMATION: antigenic peptide
US-09-815-346-9
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Query Match 100.0%; Score 43; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLVDFFLLV 9

Db 1 RLVDFFLLV 9

RESULT 2

US-09-872-832-47

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; Sequence 47, Application US/09872832
; Patent No. US20020131960A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: ARTIFICIAL ANTIGEN PRESENTING CELLS AND METHODS OF USE THEREOF
; FILE REFERENCE: 830002-2003.1
; CURRENT APPLICATION NUMBER: US/09/872,832
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 60/209,157
; PRIOR FILING DATE: 2000-02-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-872-832-47

Query Match      100.0%; Score 43; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLVDDEFLV 9
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Db 1 RLVDDEFLV 9

RESULT 3
US-09-788-110A-2
; Sequence 2, Application US/09788110A
; Publication No. US20040086518A1
; GENERAL INFORMATION:
; APPLICANT: Zanetti, Maurizio
; TITLE OF INVENTION: A Universal Vaccine and Method for Treating Cancer Employing
; FILE REFERENCE: UCSD-07017
; CURRENT APPLICATION NUMBER: US/09/788,110A
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-110A-2

Query Match      100.0%; Score 43; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLVDDEFLV 9
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Db 1 RLVDDEFLV 9

RESULT 4
US-10-080-013-35
; Sequence 35, Application US/10080013
; Publication No. US2003007248A1
; GENERAL INFORMATION:
; APPLICANT: Moriarty, Ann
; APPLICANT: Leturcq, Didier
; APPLICANT: Degraw, Juli
; APPLICANT: Heiskala, Marja
; APPLICANT: Peterson, Per
; APPLICANT: Jackson, Michael
; TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS
; FILE REFERENCE: ORT-1557
; CURRENT APPLICATION NUMBER: US/10/080,013
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
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; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-080-013-35

Query Match      100.0%; Score 43; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLVDDEFLV 9
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Db 1 RLVDDEFLV 9

RESULT 5
US-10-371-942-6
; Sequence 6, Application US/10371942
; Publication No. US2003022394A1
; GENERAL INFORMATION:
; APPLICANT: Hooogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034001
; CURRENT APPLICATION NUMBER: US/10/371,942
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,994
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-371-942-6

Query Match      100.0%; Score 43; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLVDDEFLV 9
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Db 1 RLVDDEFLV 9

RESULT 6
US-10-447-161-95
; Sequence 95, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 95
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-95

Query Match      100.0%; Score 43; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLVDDEFLV 9
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Db 1 RLVDDEFLV 9
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RESULT 7
US-10-289-566-35
; Sequence 35, Application US/10289566
; Publication No. US20040071671A1
; GENERAL INFORMATION:
; APPLICANT: Leturcq, Didier J.
; APPLICANT: Moriarty, Ann M.
; APPLICANT: Jackson, Michael R.
; APPLICANT: Peterson, Per A.
; APPLICANT: Richards, Jon M.
; TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS
; FILE REFERENCE: ORT 1342CIP
; CURRENT APPLICATION NUMBER: US/10/289,566
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/270,252
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: US 10/080,013
; PRIOR FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-289-566-35
Query Match 100.0%; Score 43; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RLVDDFLLV 9
DB 1 RLVDDFLLV 9
RESULT 8
US-10-396-578-9
; Sequence 9, Application US/10396578
; Publication No. US20040191260A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; APPLICANT: Cohen, Cyril J.
; TITLE OF INVENTION: COMPOSITIONS CAPABLE OF SPECIFICALLY BINDING PARTICULAR HUMAN
; TITLE OF INVENTION: ANTIGEN PRESENTING MOLECULE/PATHOGEN-DERIVED ANTIGEN COMPLEXES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 25563
; CURRENT APPLICATION NUMBER: US/10/396,578
; CURRENT FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: HLA-A2 restricted peptide
US-10-396-578-9
Query Match 100.0%; Score 43; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RLVDDFLLV 9
DB 1 RLVDDFLLV 9
RESULT 9
US-10-044-692-77

; Sequence 77, Application US/10044692
; Publication No. US20030096344A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,692
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-0026000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..13
; OTHER INFORMATION: /note="telomerase RT palm, primer grip
; motif C peptide from human TRT"
; SEQUENCE DESCRIPTION: SEQ ID NO: 77:
US-10-044-692-77
Query Match 100.0%; Score 43; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RLVDDFLLV 9
DB 4 RLVDDFLLV 12

RESULT 10

US-10-044-539-77
; Sequence 77, Application US/10044539
; Publication No. US20030100093A1
; GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/044,539
FILING DATE: 11-Jan-2002
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 77:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..13

OTHER INFORMATION: /note= "telomerase RT palm, primer grip motif C peptide from human TRT"

SEQUENCE DESCRIPTION: SEQ ID NO: 77:

US-10-044-539-77

Query Match 100.0%; Score 43; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLVDDELIV 9

Db 4 RLVDDELIV 12

RESULT 11

US-10-325-810-77

; Sequence 77, Application US/10325810
; Publication No. US20030204069A1
; GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 633

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/325,810
FILING DATE: 20-Dec-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/402,181
FILING DATE: 29-Sep-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 77:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..13

OTHER INFORMATION: /note= "telomerase RT palm, primer grip motif C peptide from human TRT"

SEQUENCE DESCRIPTION: SEQ ID NO: 77:

US-10-325-810-77

Query Match 100.0%; Score 43; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLVDFFLLV 9
DB 4 RLVDFFLLV 12

RESULT 12

US-10-877-146-77

; Sequence 77, Application US/10877146
; Publication No. US20050013825A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/877,146

FILING DATE: 24-Jun-2004

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/432,503

FILING DATE: 02-Nov-1999

APPLICATION NUMBER: 08/974,549

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-Apr-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-Apr-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-May-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-May-1997

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-Aug-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-Aug-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-Aug-1997

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-Oct-1997

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-Oct-1997

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph Ted

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-0026100S

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 77:

SEQUENCE CHARACTERISTICS:

; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..13
; OTHER INFORMATION: /note= "telomerase RT palm, primer grip
; motif C peptide from human TRT"
; SEQUENCE DESCRIPTION: SEQ ID NO: 77:
US-10-877-146-77

Query Match 100.0%; Score 43; DB 17; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLVDFFLLV 9
DB 4 RLVDFFLLV 12

RESULT 13

US-10-282-960-68

; Sequence 68, Application US/10282960

; Publication No. US20030143228A1

GENERAL INFORMATION:

APPLICANT: Chen, Si-Yi

APPLICANT: Zhao, You

APPLICANT: Schroers, Roland

TITLE OF INVENTION: Human Telomerase Reverse Transcriptase as a Class-II Restricted T

TITLE OF INVENTION: Associated Antigen

FILE REFERENCE: P021930S1

CURRENT APPLICATION NUMBER: US/10/282,960

CURRENT FILING DATE: 2002-10-29

PRIOR APPLICATION NUMBER: US 60/345,012

PRIOR FILING DATE: 2001-10-29

NUMBER OF SEQ ID NOS: 100

SOFTWARE: Patentin version 3.1

SEQ ID NO 68

LENGTH: 17

TYPE: PRT

ORGANISM: Human

US-10-282-960-68

Query Match 100.0%; Score 43; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLVDFFLLV 9
DB 7 RLVDFFLLV 15

RESULT 14

US-09-843-676-170

; Sequence 170, Application US/09843676

; Patent No. US20020164786A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin

Andrews, William H.

TITLE OF INVENTION: No. US20020164786A1 Telomerase

NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 19-Jan-2001
; APPLICATION NUMBER: US/09/843,676
; FILING DATE: 26-Apr-2001
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 170:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..22
; OTHER INFORMATION: /note= "motif C peptide from human
; telomerase core protein 1 (TCPl)"
; SEQUENCE DESCRIPTION: SEQ ID NO: 170:
US-09-843-676-170

Query Match 100.0%; Score 43; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLVDDEFLV 9
Db 8 RLVDDEFLV 16
|||||
|||||

RESULT 15
US-09-766-253-170
; Sequence 170, Application US/09766253
; Publication No. US20020187471A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20020187471A1el Telomerase
; NUMBER OF SEQUENCES: 171
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/766,253
; FILING DATE: 19-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,017
; FILING DATE: 1997-04-25
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002920US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 170:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..22
; OTHER INFORMATION: /note= "motif C peptide from human
; telomerase core protein 1 (TCPl)"
; SEQUENCE DESCRIPTION: SEQ ID NO: 170:
US-09-766-253-170

Query Match 100.0%; Score 43; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLVDDEFLV 9
Db 8 RLVDDEFLV 16
|||||
|||||

Search completed: May 4, 2005, 12:45:57
Job time : 92.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 12:16:58 ; Search time 24 Seconds
(without alignments)
36.081 Million cell updates/sec

Title: US-09-788-110A-2

Perfect score: 43

Sequence: 1 RLVDDEFLIV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	43	100.0	1132	2	T03844	telomerase catalyt
2	43	100.0	1611	2	T06677	hypothetical prote
3	43	100.0	1613	2	T06678	hypothetical prote
4	36	83.7	1528	2	S13743	DNA strand transfe
5	35	81.4	422	2	AD0839	probable GAB DTP g
6	35	81.4	444	2	E65045	hypothetical prote
7	35	81.4	444	2	C85913	hypothetical prote
8	35	81.4	444	2	A91069	hypothetical prote
9	35	81.4	989	2	T03838	telomerase catalyt
10	34	79.1	282	2	F83657	purine operon tran
11	34	79.1	1037	2	D96786	protein F10A5.15 [
12	34	79.1	2368	2	S46005	ESR1 protein - yea
13	33	76.7	303	2	T35930	hypothetical prote
14	33	76.7	404	2	AC2159	hypothetical prote
15	33	76.7	414	2	T08587	hypothetical prote
16	33	76.7	543	2	T35352	probable proteinas
17	33	76.7	582	2	S74819	extracellular solu
18	33	76.7	884	2	S53396	telomerase catalyt
19	33	76.7	1132	2	T31107	telomerase reverse
20	32	74.4	152	2	AG2719	conserved hypotet
21	32	74.4	152	2	C97501	hypothetical prote
22	32	74.4	346	2	F89921	threonine ammonia-
23	32	74.4	349	2	AB0950	Two-component syst
24	32	74.4	349	2	S53023	nitrogen regulatio
25	32	74.4	397	2	S76786	hypothetical prote
26	32	74.4	484	2	T19020	phosphogluconat d
27	32	74.4	592	2	F86242	unknown protein, 9
28	32	74.4	715	2	T41402	hypothetical prote
29	32	74.4	889	2	AD2215	two-component hybr

RESULT 1
T03844
telomerase catalytic chain - human
N:Alternate names: telomerase reverse transcriptase
C:Species: Homo sapiens (man)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T03844
R:Nakamura, T.M.; Morin, G.B.; Chapman, K.B.; Weinrich, S.L.; Andrews, W.H.; Lingner, J.;
Science 277, 955-959, 1997
A:Title: Telomerase catalytic subunit homologs from fission yeast and human.
A:Reference number: Z15111; MUID:97400623; PMID:9252327
A:Accession: T03844
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1132 <NAK>
A:Cross-references: UNIPROT:O14746; EMBL:AF015950; NID:g2330016; PIDN:AAC51672.1; PID:g2330016;
A:Experimental source: kidney
C:Genetics:
A:Gene: TRT
A:Map position: 5p

Query Match 100.0%; Score 43; DB 2; Length 1132;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLVDDEFLIV 9
|||
DB 865 RLVDDEFLIV 873

RESULT 2
T06677
hypothetical protein T17F15.70 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T06677
R:Quetier, F.; Choise, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattoilco, L.; Artigue
submitted to the Protein Sequence Database, April 1999
A:Reference number: Z15793
A:Accession: T06677
A:Molecule type: DNA
A:Residues: 1-1611 <QUE>
A:Cross-references: UNIPROT:Q9SU69; EMBL:AL049658; GSPDB:GN00061; ATSP:T17F15.70
A:Experimental source: cultivar Columbia; BAC clone T17F15
C:Genetics:
A:Gene: ATSP:T17F15.70
A:Map position: 3
A:Introns: 46/3; 170/3

Query Match 100.0%; Score 43; DB 2; Length 1611;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

30	32	74.4	941	2	F71332	probable chromosom
31	32	74.4	1113	2	S48495	probable membrane
32	32	74.4	3530	2	A59266	unconventional myo
33	31	72.1	99	2	H98190	hypothetical prote
34	31	72.1	176	2	D37084	enzyme of dihydrot
35	31	72.1	181	2	S40928	hypothetical prote
36	31	72.1	248	2	T23759	hypothetical prote
37	31	72.1	248	2	JC2581	14-3-3 protein - C
38	31	72.1	257	1	S13642	thyroxine deiodina
39	31	72.1	271	2	A39411	conserved hypotet
40	31	72.1	294	2	F82677	site-specific reco
41	31	72.1	303	1	S27618	5-dehydro-4-deoxyg
42	31	72.1	335	2	AH2945	fructokinase [imp
43	31	72.1	335	2	B98337	fructokinase 1 (AB
44	31	72.1	352	2	S77448	hypothetical prote
45	31	72.1	368	2	S75923	sensory transducti

ALIGNMENTS

Qy 1 RLVDDFLLV 9
| | | | |
Db 351 RLVDDFLLV 359

RESULT 3
T06678
hypothetical protein T17F15.80 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T06678
R:Quetier, F.; Choinsne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artigou
submitted to the Protein Sequence Database, April 1999
A:Reference number: Z15793
A:Accession: T06678
A:Molecule type: DNA
A:Residues: 1-1613 <QUE>
A:Cross-references: UNIPROT:Q9SU68; EMBL:AL049658; GSPDB:GN00061; ATSP:T17F15.80
A:Experimental source: cultivar Columbia; BAC clone T17F15
C:Genetics:
A:Gene: ATSP:T17F15.80
A:Map position: 3
A:Introns: 46/3; 170/3

Query Match 100.0%; Score 43; DB 2; Length 1613;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLVDDFLLV 9
| | | | |
Db 351 RLVDDFLLV 359

RESULT 4
S13743
DNA strand transferase 2 - yeast (Saccharomyces cerevisiae)
N:Alternate names: DST2 protein; KEM1 protein; protein YGL173c; RAR5 protein
C:Species: Saccharomyces cerevisiae
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C:Accession: S13743; S16701; S16885; S42156; S52457; A39790; S59238; S64190
R:Kim, J.; Ljungdahl, P.O.; Fink, G.R.
Genetics 126, 799-812, 1990
A:Title: KEM mutations affect nuclear fusion in Saccharomyces cerevisiae.
A:Reference number: S13743; MUID:91169260; PMID:2076815
A:Accession: S13743
A:Molecule type: DNA
A:Residues: 1-1528 <KIM>
A:Cross-references: UNIPROT:P22147; EMBL:X54717; NID:g3846; PIDN:CAA38520.1; PID:g3847
R:Tishkoff, D.X.; Johnson, A.W.; Kolodner, R.D.
Mol. Cell. Biol. 11, 2593-2608, 1991
A:Title: Molecular and genetic analysis of the gene encoding the Saccharomyces cerevisiae
A:Reference number: S16701; MUID:91203880; PMID:1840632
A:Accession: S16701
A:Molecule type: DNA
A:Residues: 1-1528 <MOL>
A:Cross-references: NID:g172579; PIDN:AAA35036.1; PID:g172580
R:Kipling, D.; Tambini, C.; Kearsey, S.E.
Nucleic Acids Res. 19, 1385-1391, 1991
A:Title: Rar mutations which increase artificial chromosome stability in Saccharomyces cerevisiae
A:Reference number: S16885; MUID:91227124; PMID:2027746
A:Accession: S16885
A:Molecule type: DNA
A:Residues: 1-1528 <KTP>
A:Cross-references: EMBL:X61181; NID:g4412; PIDN:CAA43487.1; PID:g4413
R:Larimer, F.W.; Stevens, A.
submitted to the EMBL Data Library, March 1992
A:Description: Structure of the XRM1 exoribonuclease gene of Saccharomyces cerevisiae.
A:Reference number: S42156
A:Accession: S42156
A:Molecule type: DNA

A:Residues: 1-1528 <LAR>
A:Cross-references: EMBL:M90097; NID:g173191; PIDN:AAA35219.1; PID:g173192
R:Bertani, I.; Coglievina, M.; Zaccaria, P.; Klima, R.; Bruschi, C.V.
submitted to the EMBL Data Library, February 1995
A:Description: The sequence of 11.1kb fragment on the left arm to Saccharomyces cerevisiae
A:Reference number: S52454
A:Accession: S52457
A:Molecule type: DNA
A:Residues: 1-1528 <BER>
A:Cross-references: EMBL:X84705; NID:g677853; PIDN:CAA59180.1; PID:g695728
R:Dykstra, C.C.; Kitada, K.; Clark, A.B.; Hamatake, R.K.; Sugino, A.
Mol. Cell. Biol. 11, 2583-2592, 1991
A:Title: Cloning and characterization of DST2, the gene for DNA strand transfer protein h
A:Reference number: A39790; MUID:91203879; PMID:1850100
A:Accession: A39790
A:Molecule type: DNA
A:Residues: 1-1260, '1', 1262-1528 <DYK>
A:Cross-references: GB:M36725
R:Bertani, I.; Coglievina, M.; Zaccaria, P.; Klima, R.; Bruschi, C.V.
Yeast 11, 1187-1194, 1995
A:Title: The sequence of an 11.1 kb fragment on the left arm of Saccharomyces cerevisiae
A:Reference number: S59235; MUID:96109931; PMID:8619317
A:Accession: S59238
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1528 <BEW>
A:Cross-references: EMBL:X84705; NID:g677853; PIDN:CAA59180.1; PID:g695728
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995
R:Bruschi, C.V.; Coglievina, M.; Bertani, I.; Klima, R.; Zaccaria, P.; Delneri, D.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64183
A:Accession: S64190
A:Molecule type: DNA
A:Residues: 1-1528 <BRU>
A:Cross-references: EMBL:Z72695; NID:gl322777; PIDN:CAA96885.1; PID:gl322778; MIPS:YGL173c
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:KEM1; DST2; SEPI; RAR5; XRM1
A:Cross-references: SGD:S0003141; MIPS:YGL173c
A:Map position: 7L
C:Superfamily: Schizosaccharomyces pombe exonuclease II
C:Keywords: nucleus

Query Match 83.7%; Score 36; DB 2; Length 1528;
Best Local Similarity 66.7%; Pred. No. 72;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLVDDFLLV 9
| : | : | : | : |
Db 276 RLVDDFLLV 284

RESULT 5
AD0839
probable GAB BTP gene cluster repressor STY2910 [imported] - Salmonella enterica subsp. C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AD0839
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, Th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AD0839
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-422 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD05899.1; PID:gl6503873; GSPDB:GN00176
C:Genetics:
A:Gene: STY2910

C:Superfamily: Escherichia coli hypothetical protein ygaF

Query Match 81.4%; Score 35; DB 2; Length 422;
Best Local Similarity 66.7%; Pred. No. 29;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLVDDFLLV 9

DB 355 KLIDDFLFV 363

RESULT 6

E65045

hypothetical protein in gapB 3'region - Escherichia coli (strain K-12)

C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C:Accession: E65045

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: E65045

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-444 <BLAT>

A:Cross-references: UNIPROT:P37339; GB:AE000351; GB:U00096; NID:gl789011; PIDN:AACT5707.

A:Experimental source: strain K-12, substrain MG1655

C:Genetics:

A:Gene: ygaF

C:Superfamily: Escherichia coli hypothetical protein ygaF

Query Match 81.4%; Score 35; DB 2; Length 444;

Best Local Similarity 66.7%; Pred. No. 31;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLVDDFLLV 9

DB 377 KLIDDFLFV 385

RESULT 7

C85913

hypothetical protein ygaF [imported] - Escherichia coli (strain O157:H7, substrain EDL93

C:Species: Escherichia coli

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C:Accession: C85913

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaesner, J.D.; Rose, D.J.; Mayhew
iller, L.; Gröbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouisis, K.; Apodaca,

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: C85913

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-444 <STO>

A:Cross-references: UNIPROT:Q8X952; GB:AE005174; NID:gl2517093; PIDN:AAGS7767.1; GSPDB:C

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: ygaF

C:Superfamily: Escherichia coli hypothetical protein ygaF

Query Match 81.4%; Score 35; DB 2; Length 444;

Best Local Similarity 66.7%; Pred. No. 31;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLVDDFLLV 9

DB 377 KLIDDFLFV 385

RESULT 8

A91069

hypothetical protein ECs3521 [imported] - Escherichia coli (strain O157:H7, substrain RIN

C:Species: Escherichia coli

C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C:Accession: A91069

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom

A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: A91069

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-444 <HAY>

A:Cross-references: UNIPROT:Q8X952; GB:BA000007; PIDN:BA836944.1; PID:gl33362992; GSPDB:G

A:Experimental source: strain O157:H7, substrain RIMD 050952

C:Genetics:

A:Gene: ECs3521

C:Superfamily: Escherichia coli hypothetical protein ygaF

Query Match 81.4%; Score 35; DB 2; Length 444;

Best Local Similarity 66.7%; Pred. No. 31;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLVDDFLLV 9

DB 377 KLIDDFLFV 385

RESULT 9

T03838

telomerase catalytic chain - fission yeast (Schizosaccharomyces pombe)

N:Alternate names: telomerase reverse transcriptase 1

C:Species: Schizosaccharomyces pombe

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C:Accession: T03838; T03839; T40085

R:Nakamura, T.M.; Morin, G.B.; Chapman, K.B.; Weinrich, S.L.; Andrews, W.H.; Lingner, J.;

Science 277, 955-959, 1997

A:Title: Telomerase catalytic subunit homologs from fission yeast and human.

A:Reference number: Z15111; MUID:97400623; PMID:9252327

A:Accession: T03838

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-989 <NAK>

A:Cross-references: UNIPROT:O13339; EMBL:AF015783; NID:g2340167; PIDN:AAC49803.1; PID:g2:

A:Experimental source: strain 972h(-)

A:Accession: T03839

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-524,526-989 <NA2>

A:Cross-references: EMBL:AF015783; NID:g2340167; PIDN:AAC49802.1; PID:g2340168

R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Volckaert, G.

submitted to the EMBL Data Library, March 1998

A:Reference number: Z21904

A:Accession: T40085

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-524,526-989 <LYN>

A:Cross-references: EMBL:AL022299; PIDN:CAA18391.1; GSPDB:GN00067; SPDB:SPBC29A3.14C

A:Experimental source: strain 972h-; cosmid c29A3

C:Genetics:

A:Gene: trt1; SPBC29A3.14C

A:Map position: 2

A:Introns: 86/3; 113/3; 153/2; 241/1; 372/1; 395/3; 485/3; 524/3; 582/2; 644/1; 693/3; 7

C:Keywords: alternative splicing

Query Match 81.4%; Score 35; DB 2; Length 989;

Best Local Similarity 66.7%; Pred. No. 72;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLVDDFLLV 9

DB 740 RVDDDFLFV 748

RESULT 10

F83657
 C:Species: Bacillus halodurans (strain C-12)
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C:Accession: F83657
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A:Reference number: A83650; MUID:20512582; PMID:11058132
 A:Accession: F83657
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-282 <STO>
 A:Cross-references: UNIPROT:Q9KGJ9; GB:AP001507; GB:BA000004; NID:g10172612; PIDN:BA8037
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: purR

Query Match 79.1%; Score 34; DB 2; Length 282;
 Best Local Similarity 77.8%; Pred. No. 30;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy

1 RLVDVFLV 9

|||||

Db 242 RLVDVFLSV 250

RESULT 11

D96786
 protein F10A5.15 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: D96786
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: D96786
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1037 <STO>
 A:Cross-references: UNIPROT:Q9LRO5; GB:AE005173; NID:g9369381; PIDN:AAF67130.1; GSPDB:GN
 C:Genetics:
 A:Gene: F10A5.15
 A:Map position: 1

Query Match 79.1%; Score 34; DB 2; Length 1037;
 Best Local Similarity 55.6%; Pred. No. 1.2e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy

1 RLVDVFLV 9

|||||

Db 331 RLVDVFLVFI 339

RESULT 12

S46005
 ESRI protein - yeast (Saccharomyces cerevisiae)
 N:Alternate names: MEC1 protein; protein YBR136W
 C:Species: Saccharomyces cerevisiae
 C:Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
 C:Accession: S46005; S46578; S46663; S47954; S64650
 R:Becam, A.M.; Herbert, C.J.; Nasr, F.; Slonimski, P.P.; Zagulski, M.
 submitted to the Protein Sequence Database, August 1994

A:Reference number: S45995

A:Accession: S46005

A:Molecule type: DNA

A:Residues: 1-2368 <BEC>

A:Cross-references: UNIPROT:P38111; EMBL:Z36005; NID:g536429; PIDN:CAA85094.1; PID:g53643

A:Experimental source: strain S288C

R:Becam, A.M.; Cullin, C.; Grzybowska, E.; Lacroute, F.; Nasr, F.; Ozier-Kalogeropoulos,

Yeast 10(Suppl.A), S1-S11, 1994

A:Title: The sequence of 29.7kb from the right arm of chromosome II reveals 13 complete c

A:Reference number: S46569; MUID:94378717; PMID:8091856

A:Accession: S46578

A:Molecule type: DNA

A:Residues: 1-2368 <BEC>

A:Cross-references: EMBL:X75891; NID:g496856; PIDN:CAA53494.1; PID:g496866

A:Experimental source: strain S288C

R:Kato, R.; Ogawa, H.

submitted to the EMBL Data Library, May 1992

A:Description: An essential gene, ESRI, is required for mitotic cell growth, DNA repair

A:Reference number: S46662

A:Accession: S46663

A:Molecule type: DNA

A:Residues: 1-196, 'D', 198-2368 <KAT>

A:Cross-references: EMBL:D11088; NID:g506874; PIDN:BA01860.1; PID:dl002337; PID:g506876

R:Kato, R.; Ogawa, H.

Nucleic Acids Res. 22, 3104-3112, 1994

A:Title: An essential gene, ESRI, is required for mitotic cell growth, DNA repair and mei

A:Reference number: S47953; MUID:94344772; PMID:8065923

A:Accession: S47954

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 195-196, 'D', 198-322; 671-744; 848-1796; 1803-2003; 2004-2368 <KAT>

A:Cross-references: EMBL:D11088

R:Weinert, T.A.; Harlow, D.

submitted to the EMBL Data Library, July 1995

A:Reference number: S64650

A:Accession: S64650

A:Molecule type: DNA

A:Residues: 1-715, 'P', 717-1254, 'Q', 1256-1275, 'G', 1277-2368 <WEI>

A:Cross-references: EMBL:U31109; NID:g950172; PIDN:AAA74482.1; PID:g950173

C:Genetics:

A:Gene: SGD:ESRI; MEC1

A:Cross-references: SGD:S0000340; MIPS:YBR136W

A:Map position: 2R

C:Function:

A:Description: required for mitotic cell growth, DNA repair, and meiotic recombination

C:Keywords: ATP; P-loop; purine nucleotide binding; transmembrane protein

F:74-90/Domain: transmembrane #status predicted <TM1>

F:218-234/Domain: transmembrane #status predicted <TM2>

F:771-787/Domain: transmembrane #status predicted <TM3>

F:922-938/Domain: transmembrane #status predicted <TM4>

F:1152-1169/Domain: transmembrane #status predicted <TM5>

F:1288-1304/Domain: transmembrane #status predicted <TM6>

F:1315-1331/Domain: transmembrane #status predicted <TM7>

F:1682-1689/Region: nucleotide-binding motif A (P-loop)

F:1918-1934/Domain: transmembrane #status predicted <TM8>

F:2126-2142/Domain: transmembrane #status predicted <TM9>

F:1688/Binding site: ATP/GTP (Lys) #status predicted

Query Match 79.1%; Score 34; DB 2; Length 2368;

Best Local Similarity 85.7%; Pred. No. 2.9e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy

1 RLVDVFL 7

|||||

Db 101 RLVDVFL 107

RESULT 13

T35930
 hypothetical protein SC9B5.10 - Streptomyces coelicolor
 C:Species: Streptomyces coelicolor
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: T35930

R;Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, January 1999
 A:Reference number: Z1551
 A:Accession: T35930
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-303 <SEE>
 A:Cross-references: UNIPROT:Q9ZBH0; EMBL:AL035206; PIDN:CAA22752.1; GSPDB:GN00070; SCOE
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: SCOE:SC995.10
 C:Superfamily: Mycobacterium tuberculosis hypothetical protein RV0731c

Query Match 76.7%; Score 33; DB 2; Length 303;
 Best Local Similarity 75.0%; Pred. No. 52;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLVDFFLL 8
 Db 86 RLVDFFLL 93

RESULT 14

AC2159
 hypothetical protein alr2826 [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp. PCC 7120
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
 C:Accession: AC2159
 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AC2159
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-404 <KUT>
 A:Cross-references: UNIPROT:Q8YV98; GB:BA000019; PIDN:BAW74525.1; PID:gl7131920; GSPDB:G
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: alr2826
 C:Superfamily: Escherichia coli hypothetical protein ygaF

Query Match 76.7%; Score 33; DB 2; Length 404;
 Best Local Similarity 66.7%; Pred. No. 71;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RLVDFFLLV 9
 Db 354 KLVDFFYIV 362

RESULT 15

T08587
 hypothetical protein L23H3.20 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C:Accession: T08587
 R;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schuel
 submitted to the Protein Sequence Database, May 1999
 A:Reference number: Z16098
 A:Accession: T08587
 A:Molecule type: DNA
 A:Residues: 1-414 <BEV>
 A:Cross-references: UNIPROT:Q9SZY8; EMBL:AL050398; GSPDB:GN00062; ATSP:L23H3.20
 A:Experimental source: cultivar Columbia; BAC clone L23H3
 C:Genetics:
 A:Gene: ATSP:L23H3.20
 A:Map position: 4
 A:Introns: 215/3; 298/3; 339/3

Query Match 76.7%; Score 33; DB 2; Length 414;

Best Local Similarity 77.8%; Pred. No. 73;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RLVDFFLLV 9
 Db 242 RLVDKFLIL 250
 Search completed: May 4, 2005, 12:29:01
 Job time : 26 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model.

Run on: May 4, 2005, 12:08:43 ; Search time 112.5 Seconds
(without alignments)
40.966 Million cell updates/sec

Title: US-09-788-110A-2

Perfect score: 43

Sequence: 1 RLVDFFLLV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_gprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	43	100.0	Q9P8T2	Q9P8T2 candida alb
2	43	100.0	Q9P8T3	Q9P8T3 candida alb
3	43	100.0	Q8NG46	Q8NG46 homo sapien
4	43	100.0	1 TERT CANFA	Q6A548 canis fami
5	43	100.0	1 TERT_HUMAN	Q14746 homo sapien
6	43	100.0	Q9SU69	Q9SU69 arabidopsis
7	43	100.0	Q9SU68	Q9SU68 arabidopsis
8	42	97.7	Q9DE32	Q9DE32 xenopus lae
9	42	97.7	Q6RD80	Q6RD80 gallus gall
10	41	95.3	Q6CSS0	Q6CSS0 kluyveromyc
11	41	95.3	Q7SD71	Q7SD71 neurospora
12	39	90.7	Q9JK99	Q9JK99 rattus norv
13	39	90.7	Q6BUF6	Q6BUF6 debaromyce
14	39	90.7	Q673L5	Q673L5 rattus norv
15	39	90.7	1 TERT_MOUSE	Q70372 mus musculu
16	39	90.7	Q673L6	Q673L6 rattus norv
17	39	90.7	Q9OXZ4	Q9OXZ4 mesocricetu
18	38	88.4	Q7SAG4	Q7SAG4 ashbya goss
19	37	86.0	Q75JF5	Q75JF5 dictyosteli
20	36	83.7	Q8PN04	Q8PN04 xanthomonas
21	36	83.7	Q8PBE9	Q8PBE9 xanthomonas
22	36	83.7	Q6ABSA4	Q6ABSA4 propionibac
23	36	83.7	Q6SXU6	Q6SXU6 euplotes ra
24	36	83.7	Q6W8T6	Q6W8T6 euplotes ra
25	36	83.7	Q6C9D0	Q6C9D0 yarrowia li
26	36	83.7	Q7Z1L0	Q7Z1L0 euplotes cr
27	36	83.7	1 KEM1_YEARST	P22147 saccharomyc
28	35	81.4	Q6SXU2	Q6SXU2 euplotes ra
29	35	81.4	Q6SXU3	Q6SXU3 euplotes eu
30	35	81.4	Q6W8T3	Q6W8T3 euplotes eu
31	35	81.4	Q69794	Q69794 raistonia s

32 35 81.4 332 2 Q9ZAZ8
33 35 81.4 336 2 Q6BLE7
34 35 81.4 367 2 Q7XSR7
35 35 81.4 416 2 Q88IT9
36 35 81.4 417 2 Q8VZ59
37 35 81.4 422 2 Q8Z4F9
38 35 81.4 422 2 Q8ZMM3
39 35 81.4 444 1 YGAF_ECOLI
40 35 81.4 444 2 Q7ABF0
41 35 81.4 444 2 Q8X9S2
42 35 81.4 444 2 Q8FES5
43 35 81.4 444 2 Q83K03
44 35 81.4 746 2 Q9FH71
45 35 81.4 813 2 Q9AST0

ALIGNMENTS

RESULT 1
Q9P8T2 PRELIMINARY; PRT; 867 AA.
AC Q9P8T2;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Telomerase reverse transcriptase 2.
GN Name=TERT2;
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
[1]
RN SEQUENCE FROM N.A.
RA Metz A.M., Love R.A., Strobel G.A., Long D.M.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF216872; AAF26733.1; -
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase.; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006278; F:RNA-dependent DNA replication; IEA.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; RVT 1; 1.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 867 AA; 100894 MW; 3273E381D5E65062 CRC64;
Query Match 100.0%; Score 43; DB 2; Length 867;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RLVDFFLLV 9
Db 664 RLVDFFLLV 672
RESULT 2
Q9P8T3 PRELIMINARY; PRT; 867 AA.
AC Q9P8T3;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Telomerase reverse transcriptase 1.
GN Name=TERT1;
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;

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RN SEQUENCE FROM N.A.
RP Metz A.M., Love R.A., Strobel G.A., Long D.M.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF216871; AAF26732.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:RNA binding; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. .; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006278; F:RNA-dependent DNA replication; IEA.
DR InterPro; IPR000477; RVase.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; RVT1; 1.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 867 AA; 100872 MW; EB67BEC54340E10F CRC64;

Query Match 100.0%; Score 43; DB 2; Length 867;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLVDFFLLV 9
Db 664 RLVDFFLLV 672

RESULT 3
Q8NG46 PRELIMINARY; PRT; 1069 AA.
AC Q8NG46;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Telomerase reverse transcriptase.
GN Name=HTRT;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN SEQUENCE FROM N.A.
RP Hisatomi H., Ohyashiki K., Ohyashiki J.H., Nagao K., Kanamaru T.,
RA Hirata H., Hibi N., Tsukada Y.;
RT "Expression profile of a gamma-deletion variant of the human
RT telomerase reverse transcriptase gene.";
RT Neoplasia 5:193-197(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Nagao K., Katsumata K., Aizawa Y., Saito N., Hirata H., Sasaki H.,
RA Yamamoto S., Hiki K., Koiwa T., Hisatomi H.;
RT "Differential alternative splicing expressions of telomerase reverse
RT transcriptase in gastrointestinal cell lines.";
RT Oncol. Rep. 11:127-131(2004).
DR EMBL; AB085628; BAC11010.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. .; IEA.
DR InterPro; IPR003545; Telomerase_RT.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase.
SQ SEQUENCE 1069 AA; 120046 MW; BE1E77A653B1C666 CRC64;

Query Match 100.0%; Score 43; DB 2; Length 1069;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLVDFFLLV 9
Db 865 RLVDFFLLV 873

RESULT 4
TERT CANFA STANDARD; PRT; 1123 AA.
AC Q6A548;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic
DE subunit).
GN Name=TERT;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15225880; DOI=10.1016/j.gene.2004.03.032;
RA Nasir L., Gault E., Campbell S., Veeramalai M., Gilbert D.,
RA McFarlane R., Munro A., Argyle D.J.;
RT "Isolation and expression of the reverse transcriptase component of
RT the Canis familiaris telomerase ribonucleoprotein (dogTERT).";
RL Gene 336:105-113(2004).
CC -!- FUNCTION: Telomerase is a ribonucleoprotein enzyme essential for
CC the replication of chromosome termini in most eukaryotes. It
CC elongates telomeres. It is a reverse transcriptase that adds
CC simple sequence repeats to chromosome ends by copying a template
CC sequence within the RNA component of the enzyme.
CC -!- SUBUNIT: Component of the telomerase ribonucleoprotein complex at
CC least composed of TEPl, EST1A, POT1 and a telomerase RNA template
CC component (TER). Interacts with PINK1 (by similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the reverse transcriptase family.
CC -!- SIMILARITY: Contains 1 reverse transcriptase domain.
CC
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CC -----
DR EMBL; AF380351; AAQ02791.1; -.
DR PROSITE; PS50878; RT POL; 1.
KW DNA-binding; Nuclear_protein; Ribonucleoprotein;
KW RNA-directed DNA polymerase; Telomere; Transferase.
FT DOMAIN 595 926 Reverse transcriptase.
SQ SEQUENCE 1123 AA; 124823 MW; F5F55D791106C1A3 CRC64;

Query Match 100.0%; Score 43; DB 1; Length 1123;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLVDFFLLV 9
Db 856 RLVDFFLLV 864

RESULT 5
TERT HUMAN STANDARD; PRT; 1132 AA.
AC O14746; O14783;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic
DE subunit) (HEST2) (Telomerase-associated protein 2) (Tp2).
GN Name=TERT; Synonyms=EST2, TCS1, TRT;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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NCBI_TaxID=9606;

[1] SEQUENCE FROM N.A.
RN TISSUE=Kidney;
RN MEDLINE=97400623; PubMed=9252327; DOI=10.1126/science.277.5328.955;
RN Nakamura T.M., Morin G.B., Chapman K.B., Weinrich S.L., Andrews W.H.,
RN Lingner J., Harley C.B., Cech T.R.;
RN "Telomerase catalytic subunit homologs from fission yeast and human.";
RN Science 277:955-959(1997).
RN [2]

SEQUENCE FROM N.A.
RN MEDLINE=97433088; PubMed=9288757; DOI=10.1016/S0092-8674(00)80538-3;
RN Meyerson M., Counter C.M., Eaton E.N., Ellisen L.W., Steiner P.,
RN Caddie S.D., Ziaugra L., Beijersbergen R.L., Davidoff M.J., Liu Q.,
RN Bacchetti S., Haber D.A., Weinberg R.A.;
RN "hEST2, the putative human telomerase catalytic subunit gene, is up-
RN regulated in tumor cells and during immortalization.";
RN Cell 90:785-795(1997).
RN [3]

SEQUENCE FROM N.A.
RN MEDLINE=99267414; PubMed=10333526; DOI=10.1016/S0378-1119(99)00108-0;
RN Wick M., Zubov D., Hagen G.;
RN "Genomic organization and promoter characterization of the gene
RN encoding the human telomerase reverse transcriptase (hTERT).";
RN Gene 232:97-106(1999).
RN [4]

SEQUENCE FROM N.A.
RN Londono-Vallejo J.A.;
RN "Sequence of a BAC carrying the entire hTERT gene.";
RN Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [5]

FUNCTION IN TELOMERASE ACTIVITY, TISSUE SPECIFICITY, ASSOCIATION WITH
RN TEPI, AND MUTAGENESIS OF ASP-868; ASP-869 AND ASP-712.
RN PubMed=9389643;
RN Harrington L., Zhou W., McPhail T., Oulton R., Yeung D.S., Mar V.,
RN Bass M.B., Robinson M.O.;
RN "Human telomerase contains evolutionarily conserved catalytic and
RN structural subunits.";
RN Genes Dev. 11:3109-3115(1997).
RN [6]

ASSOCIATION WITH TEPI.
RN PubMed=11029039;
RN Beattie T.B., Zhou W., Robinson M.O., Harrington L.;
RN "Polymerization defects within human telomerase are distinct from
RN telomerase RNA and TEPI binding.";
RN Mol. Biol. Cell 11:3329-3340(2000).
RN -!- FUNCTION: Telomerase is a ribonucleoprotein enzyme essential for
RN the replication of chromosome termini in most eukaryotes. It
RN elongates telomeres. It is a reverse transcriptase that adds
RN simple sequence repeats to chromosome ends by copying a template
RN sequence within the RNA component of the enzyme.
RN -!- SUBUNIT: Component of the telomerase ribonucleoprotein complex at
RN least composed of TEPI, ESTIA, POT1 and a telomerase RNA template
RN component (TER). Interacts with PINX1.
RN -!- SUBCELLULAR LOCATION: Nuclear.
RN -!- DISEASE: Activation of telomerase has been implicated in cell
RN immortalization and cancer cell pathogenesis.
RN -!- SIMILARITY: Belongs to the reverse transcriptase family.
RN Telomerase subfamily.
RN -!- SIMILARITY: Contains 1 reverse transcriptase domain.
RN -----

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RN -----

EMBL; AF015950; AAC51672.1; -
RN DR
EMBL; AF018167; AAC51724.1; -
RN DR
EMBL; AF128894; AAD30037.1; -
RN DR
EMBL; AF128893; AAD30037.1; JOINED
RN DR

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QY 1 RLVDFFLLV 9
Db 351 RLVDFFLLV 359

RESULT 7
Q9SU68 PRELIMINARY; PRT; 1613 AA.
AC Q9SU68;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein T17F15.80.
GN Name=T17F15.80;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Choise N., Robert C., Brottier P., Wincker P., Cattolico L., K.F.X.,
RA Artiguenave F., Saurin W., Weissenbach J., Mewes H.W., Mayer K.F.X.,
RA Lemcke K., Schueller C., Quetier F., Salanoubat M.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL049658; CAB41134.1; -.
DR FIR; T06678; T06678.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR01025; BAH.
DR InterPro; IPR010990; TFIIS conserved.
DR InterPro; IPR003617; TFS2_N.
DR Pfam; PF01426; BAH; 1.
DR SMART; SM00439; BAH; 1.
DR SMART; SM00509; TFS2N; 1.
KW Hypothetical protein.
KW SEQUENCE 1613 AA; 171987 MW; 3ADDE05E165A792 CRC64;

Query Match 100.0%; Score 43; DB 2; Length 1613;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLVDFFLLV 9
Db 351 RLVDFFLLV 359

RESULT 8
Q9DE32 PRELIMINARY; PRT; 1191 AA.
AC Q9DE32;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Telomerase reverse transcriptase.
GN Name=TERT;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21488334; PubMed=11602347; DOI=10.1016/S0378-1119(01)00684-9;
RA Kuramoto M., Ohsumi K., Kishimoto T., Ishikawa F.;
RL "Identification and analyses of the Xenopus TERT gene that encodes the
RT catalytic subunit of telomerase."
RL Gene 277:101-110(2001).

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DR EMBL; AF212299; AAG43537.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. .; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; RVT_1; 2.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 1191 AA; 138016 MW; 9BD9D776869A57D6 CRC64;

Query Match 97.7%; Score 42; DB 2; Length 1191;
Best Local Similarity 88.9%; Pred. No. 19;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLVDFFLLV 9
Db 925 RLVDFFLLV 933

RESULT 9
Q6RD80 PRELIMINARY; PRT; 1346 AA.
AC Q6RD80;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Telomerase reverse transcriptase.
GN Name=TERT;
OS Gallus gallus gallus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=208526;
RN [1]
RP SEQUENCE FROM N.A.
RA Delany M.E., Daniels L.M.;
RT "The chicken telomerase reverse transcriptase (chTERT): molecular and
RT cytogenetic characterization with a comparative analysis."
RL Gene 339:61-69(2004).
DR EMBL; AY502592; AAS75793.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. .; IEA.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; RVT_1; 1.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 1346 AA; 155316 MW; E93A8B64FB6A4D40 CRC64;

Query Match 97.7%; Score 42; DB 2; Length 1346;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLVDFFLLV 9
Db 1080 RLVDFFLLV 1088

RESULT 10
Q6CSS0 PRELIMINARY; PRT; 861 AA.
AC Q6CSS0;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)

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DE Kluyveromyces lactis strain NRRL Y-1140 chromosome C of strain NRRL Y-1140 of Kluyveromyces lactis.
GN ORFNames=KLLAOC183819;
OS Kluyveromyces lactis NRRL Y-1140.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=284590;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-1140;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Lafontaine I., de Montigny J., Marck C., Neuveglise C., Tallia E., Laffont N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V., Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C., Boisrame A., Boyer J., Catilico L., Confanier F., de Daruvar A., Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A., Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H., Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A., Swenne D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B., Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A., Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissbach J., Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-1140;
RA Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382123; CA01870.1; -;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. . .; IEA.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR010920; Sm_like_riboprot.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; RVT_1; 1.
DR PRINTS; PR01365; TELOMERASERT.
DR RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 861 AA; 100418 MW; 1C4D439782366334 CRC64;
Query Match 95.3%; Score 41; DB 2; Length 861;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RLVDFFLLV 9
Db 656 RLVDFFLLV 664
RESULT 11
Q7SD71 PRELIMINARY; PRT; 939 AA.
AC Q7SD71
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=NCU02791.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D., Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M., Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,

RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D., Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gierke S., Kamal M., Kamysellis M., Mauceli E., Bleike C., Rudd S., Frishman D., Krystofova S., Rasmussen C., Metzner R.L., Perkins D.D., Kroken S., Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A., DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R., Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R., Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M., Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
CC EMBL; AABX01000062; EAA34711.1; -;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. . .; IEA.
DR GO; GO:0006278; F:transferase activity; IEA.
DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; RVT_1; 1.
DR PRINTS; PR01365; TELOMERASERT.
DR Hypothetical protein; RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 939 AA; 104679 MW; 86F6B140E94056DC CRC64;
Query Match 95.3%; Score 41; DB 2; Length 939;
Best Local Similarity 77.8%; Pred. No. 24;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RLVDFFLLV 9
Db 900 RLVDFFLLV 908
RESULT 12
Q9JK99 PRELIMINARY; PRT; 575 AA.
AC Q9JK99
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Telomerase catalytic subunit (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22860253; PubMed=13679242; DOI=10.1016/S0024-3205(03)00670-2;
RA Wong S.C., Ong L.L., Er C.P., Gao S., Yu H., So J.B.;
RT "Cloning of rat telomerase catalytic subunit functional domains, reconstitution of telomerase activity and enzymatic profile of pig and chicken tissues.";
RL Life Sci. 73:2749-2760(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Wong S., Gao S., Xu X., Yu H.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF247818; AAF62177.1; -;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. . .; IEA.
DR GO; GO:0006278; F:transferase activity; IEA.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.

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DR Pfam; PF00078; RVT_1; 1.
KW PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase; Transferase.
FT NON TER 1
SQ SEQUENCE 575 AA; 55672 MW; F80C81BD7F6A91A3 CRC64;

Query Match 90.7%; Score 39; DB 2; Length 575;
Best Local Similarity 88.9%; Pred. No. 38;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLVDVDFLLV 9
Db 311 RFVDDFLV 319

RESULT 13
Q6BUF6 PRELIMINARY; PRT; 894 AA.
AC Q6BUF6;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Similar to sp|Q06163 Saccharomyces cerevisiae YLR18w EST2.
GN ORFNames=DEHAOC120459;
OS Debaryomyces hansenii CBS767.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
OX NCBI_TaxID=284592;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CB5767;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neugeglise C., Talia E.,
RA Goffard N., Frangeul L., Algile M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boisarane A., Boyer J., Cattolico L., Confaniolieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissensbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44 (2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CB5767;
RA Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382135; CAG86234.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. .; IEA.
DR InterPro; IPR000477; RVTse
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; RVT_1; 1.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 894 AA; 105407 MW; 37C705E712D9C8CE CRC64;

Query Match 90.7%; Score 39; DB 2; Length 894;
Best Local Similarity 77.8%; Pred. No. 58;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLVDVDFLLV 9
Db 686 RLVDVDFLVI 694

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RESULT 14
Q673L5 PRELIMINARY; PRT; 1119 AA.
AC Q673L5;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Telomerase reverse transcriptase catalytic subunit splice variant
DE a.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BN;
RA Kaneko R., Hirabayashi T., Yagi T.;
RT "Predominant expression of rTERTB, an inactive splicing variant of
RT telomerase reverse transcriptase, in the adult rat brain and heart.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY539718; AAT09125.1; -.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR InterPro; IPR003545; Telomerase_RT.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase.
SQ SEQUENCE 1119 AA; 126224 MW; 4CABB74D64E3F972 CRC64;

Query Match 90.7%; Score 39; DB 2; Length 1119;
Best Local Similarity 88.9%; Pred. No. 73;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLVDVDFLLV 9
Db 852 RFVDDFLV 860

RESULT 15
TERT MOUSE
ID TERT MOUSE STANDARD; PRT; 1122 AA.
AC Q70372; Q35432;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic
DE subunit).
DE subunit.
GN Name=Tert;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98241176; PubMed=9582020; DOI=10.1038/sj.onc.1201933;
RA Greenberg R.A., Allsopp R.C., Chin L., Morin G.B., DePinho R.A.;
RT "Expression of mouse telomerase reverse transcriptase during
RT development, differentiation and proliferation.";
RL Oncogene 16:1723-1730(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98393668; PubMed=9724727; DOI=10.1073/pnas.95.18.10471;
RA Martin-Rivera L., Herrera E., Albar J.P., Blasco M.A.;
RT "Expression of mouse telomerase catalytic subunit in embryos and adult
RT tissues.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:10471-10476(1998).
RN [3]
RP SEQUENCE OF 550-616 FROM N.A.
RA Drissi R., Cleveland J.L.;
RT "Partial sequence of Mus musculus telomerase catalytic subunit
RT homolog.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Telomerase is a ribonucleoprotein enzyme essential for
CC the replication of chromosome termini in most eukaryotes. It
CC elongates telomeres. It is a reverse transcriptase that adds

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CC simple sequence repeats to chromosome ends by copying a template
CC sequence within the RNA component of the enzyme.
CC -|- SUBUNIT: Component of the telomerase ribonucleoprotein complex at
CC least composed of TEP1, EST1A, POT1 and a telomerase RNA template
CC component (TER). Interacts with PINX1 (By similarity).
CC -|- SUBCELLULAR LOCATION: Nuclear.
CC -|- SIMILARITY: Belongs to the reverse transcriptase family.
CC Telomerase subfamily.
CC -|- SIMILARITY: Contains 1 reverse transcriptase domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF051911; AAC09323.1; -
DR EMBL; AF073311; AAC34821.1; -
DR EMBL; AF029235; AAB84200.1; -
DR MGD; MGI:1202709; Tert.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; RVT; 1.
DR PRINTS; PR01365; TELOMERASERT.
DR PROSITE; PS50878; RT_POL; 1.
KW DNA-binding; Nuclear protein; Ribonucleoprotein;
KW RNA-directed DNA polymerase; Telomere; Transferrase.
FT DOMAIN 595 928 Reverse transcriptase.
FT CONFLICT 553 553 I -> V (in Ref. 3).
SQ SEQUENCE 1122 AA; 127977 MW; F85266905DD6558C CRC64;
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Query Match 90.7%; Score 39; DB 1; Length 1122;
Best Local Similarity 88.9%; Pred. No. 73;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 RLVDDELIV 9
Db 858 RFVDDFLV 866
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